



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 113875

TO: Minh-Tam Davis
Location: Rem 3a24 / 3c18
Tuesday, February 10, 2004
Art Unit: 1642
Phone: 272-0830
Serial Number: 10 / 017066

From: Jan Delaval
Location: Biotech-Chem Library
Rem 1A51
Phone: 272-2504
jan.delaval@uspto.gov

Search Notes

priority date 10/2000
10/1999

extra search requested 02/18/04

From: Chan, Christina
Sent: Monday, February 09, 2004 2:09 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 10/017066

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Davis, Minh-Tam
Sent: Monday, February 09, 2004 12:11 PM
To: Chan, Christina
Subject: Rush search request for 10/017066

Please search in commercial database, issued patent files, PGPUB and for interference:
SEQ ID NO:1 and 2.

Thank you.

MINH TAM DAVIS
ART UNIT 1642
RESEM, ROOM 3A24, MB 3C18
272-0830

Searcher: Jan
Phone: 22504
Location: _____
Date Picked Up: 215
Date Completed: 216
Searcher Prep/Review: _____
Clerical: 10
Online time: 15

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

RECEIVED
FEB 19 2004
STIC/CHEN Division
(STIC)

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 19:20:07 ; Search time 1052 Seconds

(without alignment)
10980.867 Million cell updates/sec

Title: US-10-017-066A-1

Perfect score: 3136
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Gapex 10.0, Gapext 1.0

Searched: 2449703 seqs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3136	100.0	3136	15	US-10-001-469-2879 Sequence 2879, App
2	3136	100.0	3136	15	US-10-205-823-442 Sequence 442, App
3	3136	100.0	3136	15	US-10-225-567A-433 Sequence 433, App
4	2913.4	92.9	3104	12	US-10-295-027-872 Sequence 872, App
5	2028.4	64.7	2061	9	US-09-759-143-917 Sequence 917, App
6	2028.4	64.7	2061	9	US-09-780-669-917 Sequence 917, App
7	2028.4	64.7	2061	9	US-09-822-827-917 Sequence 917, App
8	2028.4	64.7	2061	10	US-09-895-793-917 Sequence 917, App
9	2028.4	64.7	2061	10	US-09-895-814-917 Sequence 917, App
10	2028.4	64.7	2061	13	US-10-144-678A-917 Sequence 917, App
11	2028.4	64.7	2061	13	US-10-294-025-917 Sequence 917, App
12	2028.4	64.7	2061	14	US-10-012-896-917 Sequence 917, App
13	1992.6	63.5	2034	11	US-09-966-459A-4 Sequence 4, Appl1
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45	952.4	30.4	954	13	US-10-029-386-20673 Sequence 20673, A

ALIGNMENTS

RESULT 1
US-10-001-469-2879
Sequence 2879, Application US/10001469
Publication No. US20030091562A1
GENERAL INFORMATION:
APPLICANT: JAKOBOWITS, AVA
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAFR, DANIEL
APPLICANT: SAFRAN, DOUGLAS
APPLICANT: HUBERT, RENE
APPLICANT: PARIS, MARY
APPLICANT: CHALITHA-BID, PIA
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
FILE REFERENCE: 51158-20024.20
CURRENT APPLICATION NUMBER: US/10/001,469
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/291,118
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/680,728
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2888
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2879
LENGTH: 3136
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: 101P3A11 cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: (130) .. (1083)
US-10-001-469-2879
Query Match 100.0%; Score 3136; DB 15; Length 3136;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-205-823-442
; Sequence 442, Application US/10205823

Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoerster, Sebastian
APPLICANT: Kamatkar, Shubhang
APPLICANT: Monsey, Angela M.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 442
LENGTH: 3136
TYPE: DNA
ORGANISM: Homo sapiens
US-10-205-823-442
Query Match 100.0%, Score 3136, DB 15, Length 3136,
Best Local Similarity 100.0%, Pred. No. 0,
Matches 3136, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
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Db	3121	AAAAAAAAAAAAAAAAAAAA 3136	

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RESULT 3
US-10-225-567A-433
; Sequence 433 Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 433
; LENGTH: 3136.
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-225-567A-433

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	Query Match	Similarity	Score 3136;	DB 15;	Length 3136;
	Best Local	100.0%;	Pred. No. 0;	Mismatches 0;	Gaps 0;
	Matches 3136;	Conservative	0;	Indels 0;	
QY	1 CAGAGAGGCTGTATTTCATGTCAGGCCTGCCAGACCTTTCTGGAGAGAAGCTGSA	CAAG	60		
Dd	1 CAAGAGGCTGTATTTCATGTCAGGCCTGCCAGACCTTTCTGGAGAGAAGCTGSA	CAAAG	60		
QY	61 GGGGTCACACATTCCTTCCATPAGGTTBAGCTCTACCTGCGTGCTGCTCACAGTTC		120		
Dd	61 GGGGTCACACATTCCTTCCATPAGGTTBAGCTCTACCTGCGTGCTGCTCACAGTTC		120		
QY	121 AGGCTTTATATATGATGATGCCAATGSCAAATGAATCAGATGCTCATACATTCATCCCA		180		
Dd	121 AGGCTTTATATATGATGATGCCAATGSCAATGAATCAGATGCTCATACATTCATCCCA		180		

QY	181	TTAGGACCTCCCTGGTTTAGAAGAGGCTCAGTTCTGTGTGGCTTCGCCATTGGTCTCCTC	240
Db	181	ATBAGGCTCCTGGTTTAGAAGAGGCTCAGTTCTGTGTGGCTTCGCCATTGGTCTCCTC	240
QY	241	TACCTTATGTGCTGTAGGTAACTTGACAATCATCTACATGTGGGACTGACACAGC	300
Db	241	TACCTTATGTGCTGTAGGTAACTTGACAATCATCTACATGTGGGAGTACGACACAGC	300
QY	301	CTGCATAGACCATGTATATATCTCTTGATGTCTTCAAGCATTTGACATCTCATCTCC	360
Db	301	CTGCATAGGCCATGTATATATCTTGTGATGTCTTCAAGCATTTGACATCTCATCTCC	360
QY	361	ACCTCATCCATGCCAAATATGTGGCACTCTTGTTCAATTCACCTACATCCAGTTT	420
Db	361	ACCTCATCCATGCCAAATATGTGGCACTCTTGTTCAATTCACCTACATCCAGTTT	420
QY	421	GATGCTTGTGTGCTAGACATTTTGGCCATCCACTCCTTATCTGGCATGSAATCCAGAGT	480
Db	421	GATGCTTGTGTGCTAGACATTTTGGCCATCCACTCCTTATCTGGCATGSAATCCAGAGT	480
QY	481	CTGCTGGCCATGGCTTTTGAACGGCTATGTGGCATCTGTACCACTGGCCGATGCCACA	540
Db	481	CTGCTGGCCATGGCTTTTGAACGGCTATGTGGCATCTGTACCACTGGCCGATGCCACA	540
QY	541	GTACTCTAGTGTGCTGTGTCACCAAAATGTGTGTGGCTGTGTGTGGAGGGAGGCTGCA	600
Db	541	GTACTCTAGTGTGCTGTGTCACCAAAATGTGTGTGGCTGTGTGTGGAGGGAGGCTGCA	600
QY	601	CTGATGGCAACCCCTCTCTGTCTTCATCAGCAGCTGCTCTTGCGCTCCAAATCTCTT	660
Db	601	CTGATGGCAACCCCTCTCTGTCTTCATCAGCAGCTGCTCTTGCGCTCCAAATCTCTT	660
QY	661	TCCCATTCCTACTGCTCCACACCAAGATGTATGAAGCTGGCGCTGTATGTATCTCCGACT	720
Db	661	TCCCATTCCTACTGCTCCACACCAAGATGTATGAAGCTGGCGCTGTATGTATCTCCGACT	720
QY	721	AATGTGCTATGTGGCCTTATGTCTATCATCTCCGCCATTGGCTGTGACTCATCTCTCATC	780
Db	721	AATGTGCTATGTGGCCTTATGTCTATCATCTCCGCCATTGGCTGTGACTCATCTCTCATC	780
QY	781	TCTCTTCATATCTGCTTATCTTTAAAGCTGTGTGGGCTTGACACGTGAAGCCCAAGCC	840
Db	781	TCTCTTCATATCTGCTTATCTTTAAAGCTGTGTGGGCTTGACACGTGAAGCCCAAGCC	840
QY	841	AAGSCATTTGGCACTTGCTGTCTCATGTGTGTGTGTGTGTATTTCTATATGACCTTTT	900
Db	841	AAGSCATTTGGCACTTGCTGTCTCATGTGTGTGTGTGTGTATTTCTATATGACCTTTT	900
QY	901	ATTGGAATTGTGCATGTGTGCATGTGTTTGAAGAGGGGGTGACTCCGCTGGCCCGCTATC	960
Db	901	ATTGGAATTGTGCATGTGTGCATGTGTTTGAAGAGGGGGTGACTCTCCGCTGGCCCGCTATC	960
QY	961	TTGGCCAAATCTATCTGTGTGTCTCTCTGTGTCTACCAACCAATTGTCTATGTGAAGTAA	1020
Db	961	TTGGCCAAATCTATCTGTGTGTCTCTCTGTGTCTACCAACCAATTGTCTATGTGAAGTAA	1020
QY	1021	ACAAAGAGATGTGACAGCGCATCTTTCGACTTTTTCATGTGGGCCACACAGCGTTCAAG	1080
Db	1021	ACAAAGAGATGTGACAGCGCATCTTTCGACTTTTTCATGTGGGCCACACAGCGTTCAAG	1080
QY	1081	CCCTAGGTGTAGTATCAAACTTCTTTTCCATTCAGAGTCTGTGATTCAGATTTTAAAT	1140
Db	1081	CCCTAGGTGTGTAGTATCAAACTTCTTTTCCATTCAGAGTCTGTGATTCAGATTTTAAAT	1140
QY	1141	GTTTAACTTTTGGAAAGCAGTATTCAGAAAAAAATTTCTTTATATAAAAAATCAACTCA	1200
Db	1141	GTTTAACTTTTGGAAAGCAGTATTCAGAAAAAAATTTCTTTATATAAAAAATCAACTCA	1200
QY	1201	GATCCTTCAATATGAATACTGTGGGGAATCTTCATTTTTCATATATATTTCTCTCTT	1260
Db	1201	GATCCTTCAATATGAATACTGTGGGGAATCTTCATTTTTCATATATATTTCTCTCTT	1260

QY	1261	TGTTTCTGCAACATATATATTAATACCCTGACCTAGGTTGAGGGCTATTA	1322
Db	1261	TGTTTCTGCAACATATATTAATACCCTGACCTAGGTTGAGGGCTATTA	1320
QY	1321	CTTTTCATTTTACCATGACGTCMAATCTMAA	1388
Db	1321	CTTTTCATTTTACCATGACGTCMAATCTMAA	1380
QY	1381	TGAGATPAGAATGGTACATCTGAGAAACATTTGGCCMAAGGCTTAAGCCGGAAGAA	1440
Db	1381	TGAGATPAGAATGGTACATCTGAGAAACATTTGGCCMAAGGCTTAAGCCGGAAGAA	1440
QY	1441	ATPAAACAGAAATATATATAATAGATATATACCTTAACCTTAACCTCTCTAG	1500
Db	1441	ATPAAACAGAAATATATATAATAGATATATACCTTAACCTTAACCTCTCTAG	1500
QY	1501	AACTCCCAACCAATTTGGATCTTCAGAAAATCTGTCTTCAAAATGACTTTCAGAGAA	1560
Db	1501	AACTCCCAACCAATTTGGATCTTCAGAAAATGCTGTCTTCAAAATGACTTTCAGAGAA	1560
QY	1561	GAAATATATTTTCTCTGAGACCTPAGCACTTAAGGGGAAGTGGAACTAAAGGCTTGA	1620
Db	1561	GAAATATATTTTCTCTGAGACCTPAGCACTTAAGGGGAAGTGGAACTAAAGGCTTGA	1620
QY	1621	AAAGTACATTTTACCTACGTTATGAAAATGACACACTGTCTGAGAGTTTTCACAGCA	1680
Db	1621	AAAGTACATTTTACCTACGTTATGAAAATGACACACTGTCTGAGAGTTTTCACAGCA	1680
QY	1681	TATGAACTCTGTTTCTCTATTTAATTTCTATCAACCTTTAATTAGGCAAGATTT	1740
Db	1681	TATGAACTCTGTTTCTCTATTTAATTTCTATCAACCTTTAATTAGGCAAGATTT	1740
QY	1741	ATTAGTACCTCATTTGTAAGCAGTGGAAATTGATGTTCACTGGGGAATCAGTGAATTA	1800
Db	1741	ATTAGTACCTCATTTGTAAGCAGTGGAAATTTGATGTTCACTGGGGAATCAGTGAATTA	1800
QY	1801	TGGGTCATACAGATATATAATTTAAAAAAGACCTTCATGCCAATCTCATATGA	1860
Db	1801	TGGGTCATACAGATATATAATTTAAAAAAGACCTTCATGCCAATCTCATATGA	1860
QY	1861	TGTGAAAGACGTGTAGAGAGACCAACAGGGTAGGGTTAGAGATTTCCAGAGCTTAC	1920
Db	1861	TGTGAAAGACGTGTAGAGAGACCAACAGGGTAGGGTTAGAGATTTCCAGAGCTTAC	1920
QY	1921	ATTTTCTAGAGAGATTTAATTTCTTCTACATCATCAGTGTGTATTTAGAAATTC	1980
Db	1921	ATTTTCTAGAGAGATTTAATTTCTTCTACATCATCAGTGTGTATTTAGAAATTC	1980
QY	1981	CTGGCAACAGAACTATGAGCTTTAATCCCATAGCATAGTGTATTTGTCCTGGTCCAAAT	2040
Db	1981	CTGGCAACAGAACTATGAGCTTTAATTTCCCATAGCATAGTGTATTTGTCCTGGTCCAAAT	2040
QY	2041	GCCAAATTAACCTGTGCTTTGGAAGAAGTATTTAGTTCCACATTAAGAAAGTTCTTA	2100
Db	2041	GCCAAATTAACCTGTGCTTTGGAAGAAGTATTTAGTTCCACATTAAGAAAGTTCTTA	2100
QY	2101	TTCAAGAAATGTGCAATAGGCTTTAAGCAATTTAATTTTAAAGTTCCATAGGTGA	2160
Db	2101	TTCAAGAAATGTGCAATAGGCTTTAAGCAATTTAATTTTAAAGTTCCATAGGTGA	2160
QY	2161	TTCTGATAGGCAAGTGAAGTTAGGGAGCCACAGTTATGATGGGAAGTATGGAATGGCAGG	2220
Db	2161	TTCTGATAGGCAAGTGAAGTTAGGGAGCCACAGTTATGATGGGAAGTATGGAATGGCAGG	2220
QY	2221	TCTTGAAGATTAACCTGGCTTTTGAAGTGTACATCTGCAAGTGAAGTGAAGGATCTTC	2280
Db	2221	TCTTGAAGATTAACCTGGCTTTTGAAGTGTACATCTGCAAGTGAAGTGAAGGATCTTC	2280
QY	2281	AGGACCAATGCTTTAATTTGGGCTTTTGCAAGTATGGAACAGGACTTTGAGACCAAGAAA	2340
Db	2281	AGGACCAATGCTTTAATTTGGGCTTTTGCAAGTATGGAACAGGACTTTGAGACCAAGAAA	2340
QY	2341	GCAATTCGACTTAGGCAATGGGAATCAGGCAATTTTGCTTCTGAGGGGCTATTTACAAAGG	2400

Db	2341	GCANCTGACCTTAGGCATGGGAATCAAGGCATTTTGGCTTCTGAGGGCTATTACCAAGG	2400
Qy	2401	TTAATAGGTTTCATCTTCACAGGATATGACACAGTGTTPACCAAGAACTCAATTAC	2460
Db	2401	TTAATAGGTTTCATCTTCACAGGATATGACACAGTGTTPACCAAGAACTCAATTAC	2460
Qy	2461	AAATACATAACATGTGATCATATATGGTAAGTTCAATTCCTTTTCAATCCACAG	2520
Db	2461	AAATACATAACATGTGATCATATATGGTAAGTTCAATTCCTTTTCAATCCACAG	2520
Qy	2521	TTCCCTGATATGATATCCATATPACATGCTTCATCCCTTTTGTATGATATCATATT	2580
Db	2521	TTCCCTGATATGATATCCATATPACATGCTTCATCCCTTTTGTATGATATCATATT	2580
Qy	2581	GGAAATGGCTATTTAATATCTGTATTTTGGCTGGAGATGTAAAGCCATGAGGGCAGTGT	2640
Db	2581	GGAAATGGCTATTTAATATCTGTATTTTGGCTGGAGATGTAAAGCCATGAGGGCAGTGT	2640
Qy	2641	TATATTGAATGATCTGTCTGTTCATGACAGTGCCTTTGCTCATCATTTGATCCCC	2700
Db	2641	TATATTGAATGATCTGTCTGTTCATGACAGTGCCTTTGCTCATCATTTGATCCCC	2700
Qy	2701	AGCAAAAGCTCTAATAATATATGCTTTATGCTTGAACACCGGTATTTTCAATCAACC	2760
Db	2701	AGCAAAAGCTCTAATAATATATGCTTTATGCTTGAACACCGGTATTTTCAATCAACC	2760
Qy	2761	TGATTCCTCTGTCTCTGAACACATAGCCAGGCAATTTCCAGGCTTCTTGAGTGGGTA	2820
Db	2761	TGATTCCTCTGTCTCTGAACACATAGCCAGGCAATTTCCAGGCTTCTTGAGTGGGTA	2820
Qy	2821	TTATTTAATTTCTGGCCATTAATCTTCGAAATGTGAGTGAAGTGAATGTGCAATTTCTATAC	2880
Db	2821	TTATTTAATTTCTGGCCATTAATCTTCGAAATGTGAGTGAAGTGAATGTGCAATTTCTATAC	2880
Qy	2881	CTGGCTCATATAAAACCCCTCCCATGGCAGCCTTTCACTGATGACATTAATGTGACTGGGA	2940
Db	2881	CTGGCTCATATAAAACCCCTCCCATGGCAGCCTTTCACTGATGACATTAATGTGACTGGGA	2940
Qy	2941	AGCTATGTGTACACAGAGTAAATCAACAGAACCTGATTTCTGAAAAAATCTGTCCAG	3000
Db	2941	AGCTATGTGTACACAGAGTAAATCAACAGAACCTGATTTCTGAAAAAATCTGTCCAG	3000
Qy	3001	GCCAAACCTCTGTCTATTGCAATCTCCCATTTGATTTGTAACGAGGCACTTGATTAAGTGA	3060
Db	3001	GCCAAACCTCTGTCTATTGCAATCTCCCATTTGATTTGTAACGAGGCACTTGATTAAGTGA	3060
Qy	3061	AAATTAAGTACTATTGTCTCAAGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3120
Db	3061	AAATTAAGTACTATTGTCTCAAGAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3120
Qy	3121	AAAAAAAAAAAAAAAAAAAA 3136	
Db	3121	AAAAAAAAAAAAAAAAAAAA 3136	


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FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 872
LENGTH: 3104
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(3104)
OTHER INFORMATION: n = g, a, c or t
US-10-295-027-872

Query Match          92.9%; Score 2913.4; DB 12; Length 3104;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2946; Conservative 1; Mismatches 18; Indels 3; Gaps 2;

QY 1 CAGAGAGGCTGTAATTCAGTGCAGCCTGCGACAGCTCTTTGGAGGAAGATCGACAAAG 60
DB 1 CAGAGAGGCTGTAATTCAGTGCAGCCTGCGACAGCTCTTTGGAGGAAGATCGACAAAG 60
QY 61 GGGGTACACATTCCTTCATAGGTTGAGGCTGACCTGACCTGAGTGTGTCACAGTTTC 120
DB 61 GGGGTACACATTCCTTCATAGGTTGAGGCTGACCTGACCTGAGTGTGTCACAGTTTC 120
QY 121 AGCTTCTCATATGATGATGATCCCAATGGAATGCAATGATGATGATGATGATGATGAT 180
DB 121 AGCTTCTCATATGATGATGATCCCAATGGAATGCAATGATGATGATGATGATGATGAT 180
QY 181 ATAGGCTCTGCTGTTTAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 ATAGGCTCTGCTGTTTAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 TACCTTATGCTGTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
DB 241 TACCTTATGCTGTGTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 301 CTGCAATGAGCCCAATGATATATTTCTTTCAGATGATGATGATGATGATGATGATGATGAT 360
DB 301 CTGCAATGAGCCCAATGATATATTTCTTTCAGATGATGATGATGATGATGATGATGATGAT 360
QY 361 ACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 ACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 GATGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 GATGCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 CTGCTGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

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DB 481 CTGCTGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 GATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 GATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CTGATGAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 601 CTGATGAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 661 TCCCATCTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 TCCCATCTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 AATGCTGCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB 721 AATGCTGCTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TCCCTTCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 781 TCCCTTCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 AAGGCTATTTGGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 841 AAGGCTATTTGGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 ATTGATTTGTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 901 ATTGATTTGTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TTGGCCATATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 961 TTGGCCATATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 ACAAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 ACAAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CCTTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 CCTTAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 GTTAACTATTTGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 GTTAACTATTTGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1141 GTTAACTATTTGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
DB 1141 GTTAACTATTTGAGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
QY 1201 GATCTTCAAAATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 GATCTTCAAAATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 CTCTTCAATTTTACATGAGTCCAAATCTAAATCTGCTTCTACTGATGATGATGATGATGATGATGATGAT 1380
DB 1321 CTCTTCAATTTTACATGAGTCCAAATCTAAATCTGCTTCTACTGATGATGATGATGATGATGATGATGAT 1380
QY 1320 CTCTTCAATTTTACATGAGTCCAAATCTAAATCTGCTTCTACTGATGATGATGATGATGATGATGATGAT 1379
DB 1320 CTCTTCAATTTTACATGAGTCCAAATCTAAATCTGCTTCTACTGATGATGATGATGATGATGATGATGAT 1379
QY 1381 TGAATTAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
DB 1381 TGAATTAAGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1441 ATAAAGCAAGATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1500
DB 1441 ATAAAGCAAGATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1500
QY 1501 AACTCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
DB 1501 AACTCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 1500 AACTCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1559
DB 1500 AACTCCCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1559
QY 1561 GAATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB 1561 GAATTAATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

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QY	1209	AAATATGAACCGTGTGGGGAATCCCAATTTTTCATATATATTTCTCTTGTTTCT	1268
Db	182	AAATATGAACCTGGTGTGGGAATCTCCATTTTTCATATATATTTCTCTTGTTTCT	241
QY	1269	TGCTACATATATATTTAATACCCCTAGTAGGTGTGTGGAGGATTAATCTTTTCAT	1328
Db	242	TGCTACATATATATTTAATACCCCTAGCTAGGTGTGTGTGGAGGATTAATCTTTTCAT	301
QY	1329	TTTACCATGACGTCCCAATCTTAACTGTCTTCTACATAGTTTACAGATTTCTGAGATTA	1388
Db	302	TTTACCATGACGTCCCAATCTTAACTGTCTTCTACATAGTTTACAGATTTCTGAGATTA	361
QY	1389	GAATGTACATCTAGAGAACATTTTGCCAAGGCGCTTAACACGGCACAAAGAAATTAACAC	1448
Db	362	GAATGTACATCTAGAGAACATTTTGCCAAGGCGCTTAACACGGCACAAAGAAATTAACAC	421
QY	1449	AGAAATATATATTAATGAATATATCTAGTTAAACTATTAATCTTCTCTTCAGAACTCCCA	1508
Db	422	AGAAATATATATTAATGAATATATCTAGTTAAACTATTAATCTTCTCTTCAGAACTCCCA	481
QY	1509	ACCACATTTGATCTCAGAAAAATGTGTCTTCAAAAATAGACTTTCACAGAGAAATATAT	1568
Db	482	ACCACATTTGATCTCAGAAAAATGTGTCTTCAAAAATAGACTTTCACAGAGAAATATAT	541
QY	1569	TTTTCTCTGACACATGACCTTAAAGGGAAGATTGAAAGTAAACCTTGAAGAAAGATAC	1628
Db	542	TTTTCTCTGACACCTAGCACTTAAAGGGAAGATTGAAAGTAAACCTTGAAGAAAGATAC	601
QY	1629	ATTATACCTAGCTTATGAAAGTGTGACACACTGTTCTGAGATTTTCACAGATATGACCC	1688
Db	602	ATTATACCTAGCTTATGAAAGTGTGACACACTGTTCTGAGATTTTCACAGATATGACCC	661
QY	1689	CTGTATTTTCTATTTAATTTTCTTATCAACCCCTTAAATTAGCAAGATATTTATTAGTAC	1748
Db	662	CTGTATTTTCTATTTAATTTTCTTATCAACCCCTTAAATTAGCAAGATATTTATTAGTAC	721
QY	1749	CCTCATTTGACCATGGAAAAATTGATGTCACTGTGGGATCACTGAAATTAATGGGCTCA	1808
Db	722	CCTCATTTGACCATGGAAAAATTGATGTCACTGTGGGATCACTGAAATTAATGGGCTCA	781
QY	1809	TACAAAGTAAATAATTAATAAAAAAAAAAGCTTATGCGCAATCTCATATATGTGAGAG	1868
Db	782	TACAAAGTAAATAATTTT - AAAAAAAAAAGACTTATGCGCAATCTCATATATGTGAGAG	839
QY	1869	AACTGTATGAGAGACCAACAGGGTATGTGGTTAGAGATTTCCAGAGTCTTACATTTCTA	1928
Db	840	AACTGTATGAGAGACCAACAGGGTATGTGGTTAGAGATTTCCAGAGTCTTACATTTCTA	899
QY	1929	GAGGAGGATTTAATTTCTTCTCATCTCATCCAGTGTCTAATTTAGGAATTTCCGCGAAC	1988
Db	900	GAGGAGGATTTAATTTCTTCTCATCTCATCCAGTGTCTAATTTAGGAATTTCCGCGAAC	959
QY	1989	AGAACTCAGGCTTTAATCCCACTAGCTATTTGCTTATGTCCTGTCGAATTTGCCAATTA	2048
Db	960	AGAACTCAGGCTTTAATCCCACTAGCTATTTGCTTATGTCCTGTCGAATTTGCCAATTA	1019
QY	2049	CCGTGTCTTGGAAAGAAAGTGAATTTCTTAGGTCAACCATTAATGGAAGATTTCTTACAGAA	2108
Db	1020	CCGTGTCTTGGAAAGAAAGTGAATTTCTTAGGTCAACCATTAATGGAAGATTTCTTACAGAA	1079
QY	2109	GTCGTCAATAGGCGTTATAGCAAGTATATTTTATTAAGTTCCATAGGTGATTTCTGATA	2168
Db	1080	GTCGTCAATAGGCGTTATAGCAAGTATATTTTATTAAGTTCCATAGGTGATTTCTGATA	1139
QY	2169	GGCAGTGAAGTTAGAGAACCAACAGTTATGATGGAAGATGAAATGCGACGCTTGAAG	2228
Db	1140	GGCAGTGAAGTTAGAGAACCAACAGTTATGATGGAAGATGAAATGCGACGCTTGAAG	1199
QY	2229	ATAACATTTGGCGTTTGTAGTGTGACTGTACTGTGAAAAGTGAAGGAATCTTCAAGACAT	2288
Db	1200	ATAACATTTGGCGTTTGTAGTGTGACTGTACTGTGAAAAGTGAAGGAATCTTCAAGACAT	1259
QY	2289	GCTTTATTTGGGCGTTTGTGTGCAGTATGGAACAGGGAACCTTTGAGACAGAGAAAGCAATCTG	2348

Db	1260	GCTTAAATGGGGCTTGTGTGACATATGAAACAGGACCTTTAGACCAAGAAACGAACTGTG	1315
Qy	2349	ACTTAGGCATGGGAATCAGGCATTTTGGCTTCTGAGGGGCTATTACCAAGGGTTAAATAG	2408
Db	1320	ACTTAGGCATGGGAATCAGGCATTTTGGCTTCTGAGGGGCTATTACCAAGGGTTAAATAG	1379
Qy	2409	TTTTCATCTTTCACAGGATATGACACAGTGTAAACCAAGAACTCAATTACAAATACTA	2466
Db	1380	TTTCATCTTTCACAGGATATGACACAGTGTAAACCAAGAACTCAATTACAAATACTA	1433
Qy	2469	AAACATGATCATATATATGTGTAAAGTTTCATTTCTTTTCAATCCCTCAGGTTCCCTGA	2528
Db	1440	AAACATGATCATATATATGTGTAAAGTTTCATTTCTTTTCAATCCCTCAGGTTCCCTGA	1499
Qy	2529	TATGGATTCTCATTAACATGCTTTTCATCCCTTTTGTAAATGGATATCATATTTGGAAATGC	2588
Db	1500	TATGGATTCTCATTAACATGCTTTTCATCCCTTTTGTAAATGGATATCATATTTGGAAATGC	1555
Qy	2589	CTATTTAATCTGTGATTTTGTGTGTGACACGTAGGCCCAAGAGGGCCTGTTTATATAG	2644
Db	1560	CTATTTAATCTGTGATTTTGTGTGTGACACGTAGGCCCAAGAGGGCCTGTTTATATAG	1618
Qy	2649	AATGTCAATCTCTGTTCATCATTTGACCTGCTCTTGTCTCATCATTTGAATCCCCAGCAAGT	2708
Db	1620	AATGTCAATCTCTGTTCATCATTTGACCTGCTCTTGTCTCATCATTTGAATCCCCAGCAAGT	1679
Qy	2709	GCCTAGAACATATATATGTGCTTATGTCTTGACACCGGTTATTTTTCATCAAACTGTATCCT	2768
Db	1680	GCCTAGAACATATATATGTGCTTATGTCTTGACACCGGTTATTTTTCATCAAACTGTATCCT	1739
Qy	2769	TCTGTCTCTGAACACATATGACCAAGCAATTTTCCAGCCTCTTGTAGTGGGATATTATPAA	2828
Db	1740	TCTGTCTCTGAACACATATGACCAAGCAATTTTCCAGCCTCTTGTAGTGGGATATTATPAA	1799
Qy	2829	TTCTGGCCATTAATCTCCATATGTGATGTGAAGTGAACATGTGCATTTCTATACCTGGCTCA	2888
Db	1800	TTCTGGCCATTAATCTCCATATGTGATGTGAAGTGAACATGTGCATTTCTATACCTGGCTCA	1855
Qy	2889	TAAAAACCTCCCATATGTGACAGCCTTTCATGTGTGACATTAATATGTGATGGGAAGCTATGT	2948
Db	1860	TAAAAACCTCCCATATGTGACAGCCTTTCATGTGTGACATTAATATGTGATGGGAAGCTATGT	1919
Qy	2949	GTTACACAGATTAATATCACCAGAAAGCCTGTGATTTCTGAAAAAACTGTGCAGAGCCAAAC	3008
Db	1920	GTTACACAGATTAATATCACCAGAAAGCCTGTGATTTCTGAAAAAACTGTGCAGAGCCAAAC	1979
Qy	3009	TCTGTCAATTTTGCACTCCCACTGTATTTGTAGAGGACAGTGTGAATAGTAAGTAATAATPAA	3068
Db	1980	TCTGTCAATTTTGCACTCCCACTGTATTTGTAGAGGACAGTGTGAATAGTAAGTAATAATPAA	2039
Qy	3069	GTACTATTGTGTCAAG 3084	
Db	2040	GTACTATTGTGTCAAG 2055	

QY	2589	TTATTTAATTAAGTGAATTTGCTGCTGAGACTGAAGCCATGAAGGCACTGTTTATTTATG	2648
Db	1560	CTATTTAATTAAGTGAATTTGCTGCTGAGACTGAAGCCATGAAGGCACTGTTTATTTATG	1619
QY	2649	AATGCACTCTGTTCAATATTTGACTGCTCTTTGCTCATCATGTAATCCCCAGCAAGT	2708
Db	1620	AATGCACTCTGTTCAATATTTGACTGCTCTTTGCTCATCATGTAATCCCCAGCAAGT	1679
QY	2709	GCGTGAACATTAATGAGCTTAATGTTGAACCCGGTATTTTTCAATCAACCTGATTCCT	2768
Db	1680	GCGTGAACATTAATGAGCTTAATGTTGAACCCGGTATTTTTCAATCAACCTGATTCCT	1739
QY	2769	TCTGCTCGAACACATATAGCCAGCAATTTTCCAGGCTTCTTTAGTGGGTATTTATTA	2828
Db	1740	TCTGCTCGAACACATATAGCCAGCAATTTTCCAGGCTTCTTTAGTGGGTATTTATTA	1799
QY	2829	TTCTGCGCATTAATCTTCCATATGTAAGTGAAGTGAATGACATGCAATTTCTATACCTGCTCA	2888
Db	1800	TTCTGCGCATTAATCTTCCATATGTAAGTGAAGTGAATGACATGCAATTTCTATACCTGCTCA	1859
QY	2889	TAAACCTCCCATATGTCAGGCTTTCATGTTGAACATTAATGTCATTTGGAAGCTATGT	2948
Db	1860	TAAACCTCCCATATGTCAGGCTTTCATGTTGAACATTAATGTCATTTGGAAGCTATGT	1919
QY	2949	GTTACACAGAGTAATCAACAGAAAGCTGATTTCTGAAAAAAGCTGTGACAGCCAAAC	3008
Db	1920	GTTACACAGAGTAATCAACAGAAAGCTGATTTCTGAAAAAAGCTGTGACAGCCAAAC	1979
QY	3009	TCTGTCATTTGCAACTCCCACTGTTATTTGACAGGAGGATGATGAATGAATGAATTA	3068
Db	1980	TCTGTCATTTGCAACTCCCACTGTTATTTGACAGGAGGATGATGAATGAATGAATTA	2039
QY	3069	GTAATTTGTTGTCAG 3084	
Db	2040	GTAATTTGTTGTCAG 2055	
RESULT 8			
US-09-895-793-917			
Sequence 917, Application US/09895793			
Publication No. US20020192763A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Devin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan L.			
APPLICANT: Jieng, Yugu			
APPLICANT: Kalos, Michael D.			
APPLICANT: Retter, Marc W.			
APPLICANT: Stolk, John A.			
APPLICANT: Day, Craig H.			
APPLICANT: Vedvick, Thomas S.			
APPLICANT: Carter, Darick			
APPLICANT: Li, Samuel X.			
APPLICANT: Wang, Aijun			
APPLICANT: Skeiky, Yasir A.W.			
APPLICANT: Hepler, William T.			
APPLICANT: Henderson, Robert A.			
APPLICANT: McNeill, Patricia D.			
APPLICANT: Houghton, Raymond L.			
APPLICANT: Vinals de Bassols, Carlota			
APPLICANT: Foy, Teresa			
APPLICANT: Fanger, Gary R.			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE REFERENCE: 210121.534C2			
CURRENT APPLICATION NUMBER: US/09/895,793			
CURRENT FILING DATE: 2001-06-29			
NUMBER OF SEQ ID NOS: 982			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 917			

	LENGTH: 2061	TYPE: DNA	ORGANISM: Homo sapiens	US-09-895-793-917
Query Match	64.7%	Score 2028.4	DB 10	Length 2061
Best Local Similarity	99.8%	Pred. No. 0		
Matches 2052	Conservative 0	Mismatches 1	Indels 3	Gaps 2
QY	1029	GATTCGACAGGCGATCCCTTGACATCTTTCGCATGTGCGCACACAGCCTTCAGAGCCCTAGT	1088	
DB	3	GATTCGACAGGCGATCCCTTGACATCTTTCGCATGTGCGCACACAGCCTTCAGAGCCCTAGT	62	
QY	1089	GTCGATGATCAAACTTCCTTCCATTCAGAGTCCTGATTCAGATTTTAATGTAAACAT	1148	
DB	63	GTCGATGATCAAACTTCCTTCCATTCAGAGTCCTGATTCAGATTTTAATGTAAACAT	122	
QY	1149	TTTGGAAAGACAGTATTCAAAAAAAATTTCTTAATPAAAAATCAACTCAGATCCTTC	1208	
DB	123	TTTGGAAAGACAGTATTCAAAAAAAATTTCTTAATPAAAAATCAACTCAGATCCTTC	181	
QY	1209	AAATATGAAAATCGGTGGGGAATCTCAATTTTTCAATATATTTCTCTTTGGTTTCT	1266	
DB	182	AAATATGAAAATCGGTGGGGAATCTCAATTTTTCAATATATTTCTCTTTGGTTTCT	241	
QY	1269	TGCTACATATATATTTAATTAATACCTGACATGAGTTGTGTTGGAGGGTTATTAATCTTTCAT	1328	
DB	242	TGCTACATATATATTTAATTAATACCTGACATGAGTTGTGTTGGAGGGTTATTAATCTTTCAT	301	
QY	1329	TTTACGATGAGGTCCTCAATCTAAACAGCTCTCTACATAGGTTTACAGCATTCAGATTA	1388	
DB	302	TTTACGATGAGGTCCTCAATCTAAACAGCTCTCTACATAGGTTTACAGCATTCAGATTA	361	
QY	1389	GAATGTACATCTAGAGACATTTGCCAAAGCCTTAAGACAGGCAAGAAATTAACAC	1448	
DB	362	GAATGTACATCTAGAGACATTTGCCAAAGCCTTAAGACAGGCAAGAAATTAACAC	421	
QY	1449	AGATTAATTAATTAATGATATATCTAGCTTAATTAATTAATCTCTCTTCAAGATCTCCA	1508	
DB	422	AGATTAATTAATTAATGATATATCTAGCTTAATTAATTAATCTCTCTTCAAGATCTCCA	481	
QY	1509	ACCAATTTGATCTCAGAAAAATGCTGTCTTCAAAATGATCTTACAGAGAGAAATTAAT	1568	
DB	482	ACCAATTTGATCTCAGAAAAATGCTGTCTTCAAAATGATCTTACAGAGAGAAATTAAT	541	
QY	1569	TTTTCCCTCTGAGACATTAAGGGAAGATTTGAATTAAGCCTTGAAGAAATGATAC	1628	
DB	542	TTTTCCCTCTGAGACATTAAGGGAAGATTTGAATTAAGCCTTGAAGAAATGATAC	601	
QY	1629	ATTATCCATGATTAATGAAGTTGACACATGTTCTGAGAGTTTTCACACATATGAGCC	1688	
DB	602	ATTATCCATGATTAATGAAGTTGACACATGTTCTGAGAGTTTTCACACATATGAGCC	661	
QY	1689	CTGTTTTTCTATTTAATTTTCTTATCAACCTTTTAATTGCGAAAGATTAATTAAGTAC	1748	
DB	662	CTGTTTTTCTATTTAATTTTCTTATCAACCTTTTAATTGCGAAAGATTAATTAAGTAC	721	
QY	1749	CCTCATTTGATGAGGAAATTTGATGTTCACTGGGATCAGTGAATTAATGAGGCTCA	1808	
DB	722	CCTCATTTGATGAGGAAATTTGATGTTCACTGGGATCAGTGAATTAATGAGGCTCA	781	
QY	1809	TACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1868	
DB	782	TACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	839	
QY	1869	AACGTGTAGAGACCAACAGGCTAGGCTGTAGAGATTTCCAGAGTCTTAATTTTCTA	1928	
DB	840	AACGTGTAGAGACCAACAGGCTAGGCTGTAGAGATTTCCAGAGTCTTAATTTTCTA	899	
QY	1929	GAGAGATTAATTAATTTCTTCTACATCTCAGTGTGTATTTAGAAATTTCTGCGAAC	1988	
DB	900	GAGAGATTAATTAATTTCTTCTACATCTCAGTGTGTATTTAGAAATTTCTGCGAAC	959	

QY 1989 AGAAGTCTGAGGCTTTATATCCCACTAGCTATGCTTATGCTGCTGCTCAATGCGCAATTA 2048
 DB 960 AGAAGTCTGAGGCTTTATATCCCACTAGCTATGCTTATGCTGCTGCTCAATGCGCAATTA 1019
 QY 2049 CCTGTGCTTGGAGAGAGATTTCTAGGTCACATTAATGAGAGATTTCTTATTCAGAA 2108
 DB 1020 CCGTGTCTTGGAGAGAGATTTCTAGGTCACATTAATGAGAGATTTCTTATTCAGAA 1079
 QY 2109 GTCTGCAATAGGCTTATAGCAAGTATTTATTTTAAAGTTCATAGGTGATTCGATA 2168
 DB 1080 GTCTGCAATAGGCTTATAGCAAGTATTTATTTTAAAGTTCATAGGTGATTCGATA 1139
 QY 2169 GGAAGTAGGTTAGGAGGCAACAGTATGATGGAGATGGAATGGAAGGCTTTGAAG 2228
 DB 1140 GGAAGTAGGTTAGGAGGCAACAGTATGATGGAGATGGAATGGAAGGCTTTGAAG 1199
 QY 2229 ATAAATGAGCTTTGAGTGTAGTCTGTAGTGAAGAGGAGATCTTCAGACAT 2288
 DB 1200 ATAAATGAGCTTTGAGTGTAGTCTGTAGTGAAGAGGAGATCTTCAGACAT 1259
 QY 2289 GCTTTATTTGGGCTTTGTGCAATGAAACAGGACTTTGAGACCAAGAAACCAATCTG 2348
 DB 1260 GCTTTATTTGGGCTTTGTGCAATGAAACAGGACTTTGAGACCAAGAAACCAATCTG 1319
 QY 2349 ACTTAGGATGGAATCAGGCAATTTTGTCTGAGGAGGCTATACCAAGGCTTATAGG 2408
 DB 1320 ACTTAGGATGGAATCAGGCAATTTTGTCTGAGGAGGCTATACCAAGGCTTATAGG 1379
 QY 2409 TTTTATTTCAAGAGATATGACACAGTGTAAACCAAGAACTCAATTAACAAATCTA 2468
 DB 1380 TTTTATTTCAAGAGATATGACACAGTGTAAACCAAGAACTCAATTAACAAATCTA 1439
 QY 2469 AAACATGTATCATATATGTGTATGATTCATTTCTTTTCAATCAGGCTTATTCCTGA 2528
 DB 1440 AAACATGTATCATATATGTGTATGATTCATTTCTTTTCAATCAGGCTTATTCCTGA 1499
 QY 2529 TATGATTTCTTATACATATGCTTTCATCCCTTTGTATGATATCATATTTGAAATGC 2588
 DB 1500 TATGATTTCTTATACATATGCTTTCATCCCTTTGTATGATATCATATTTGAAATGC 1559
 QY 2589 CTATTTATATCTGTATTTGCTGCTGCACTGTATAGCCCACTGAGGAGCTTTATTTG 2648
 DB 1560 CTATTTATATCTGTATTTGCTGCTGCACTGTATAGCCCACTGAGGAGCTTTATTTG 1619
 QY 2649 AATGTCATCTGCTTATCATCTGCTGCTTGTGCTCATCATTTGAATCCCAAGCAAGT 2708
 DB 1620 AATGTCATCTGCTTATCATCTGCTGCTTGTGCTCATCATTTGAATCCCAAGCAAGT 1679
 QY 2709 GCTTGAACATATATGCTTATGCTTGAACCCGTTATTTTCATCAAACTGATTCCT 2768
 DB 1680 GCTTGAACATATATGCTTATGCTTGAACCCGTTATTTTCATCAAACTGATTCCT 1739
 QY 2769 TCTGTCTGAGACATAGCAGGCAATTTTCAGGCTTCTTTGAGTGGGATTTATTA 2828
 DB 1740 TCTGTCTGAGACATAGCAGGCAATTTTCAGGCTTCTTTGAGTGGGATTTATTA 1799
 QY 2829 TTTGTGCAATTAATTCATGATGATGAGATGACATGCAATTTCTATACCTGCTCA 2888
 DB 1800 TTTGTGCAATTAATTCATGATGATGAGATGACATGCAATTTCTATACCTGCTCA 1859
 QY 2889 TAAATCCCTCCCATGAGGCTTTCATGATGATGATGATGATGATGATGATGATGATGAT 2948
 DB 1860 TAAATCCCTCCCATGAGGCTTTCATGATGATGATGATGATGATGATGATGATGATGAT 1919
 QY 2949 GTTACACAGATTAATCAGGAGAGCTGATTTCTGAATTAATCTGTGACAGCAACCC 3008
 DB 1920 GTTACACAGATTAATCAGGAGAGCTGATTTCTGAATTAATCTGTGACAGCAACCC 1979
 QY 3009 TCTGTATTTGGCACTTCCCATTTGTATTTGTAGAGAGGCTTGTAGATGATGATGATGAT 3068
 DB 1980 TCTGTATTTGGCACTTCCCATTTGTATTTGTAGAGAGGCTTGTAGATGATGATGATGAT 2039
 QY 3069 GTACTATTTGTGTCAG 3084

DB 2040 GTACTATTTGTGTCAG 2055
 RESULT 9
 US-09-895-814-917
 ; Sequence 917, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurst, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Baesols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C26
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 990
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 917
 ; LENGTH: 2061
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-895-814-917
 Query Match 64.7%; Score 2028.4; DB 10; Length 2061;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
 QY 1029 GATTGACAGGCAATCTTGCATTTTCATGTGACACACAGCTTCAGAGCCCTAGT 1088
 DB 3 GATTGACAGGCAATCTTGCATTTTCATGTGACACACAGCTTCAGAGCCCTAGT 62
 QY 1089 GTGCTATCAAACTTCTTTCATTCAGAGTCTGATTCAGATTTTATGTTAATCAT 1148
 DB 63 GTGCTATCAAACTTCTTTCATTCAGAGTCTGATTCAGATTTTATGTTAATCAT 122
 QY 1149 TTTGAGACAGATTCAGAAAAAAATTTCTTATTAATTAATTAATTAATTAATTAATTAAT 1208
 DB 123 TTTGAGACAGATTCAGAAAAAAATTTCTTATTAATTAATTAATTAATTAATTAATTAAT 181
 QY 1209 AAAATATGAATGCTTGGGAGATTCATTTTTCATATATATTTCTTTGTTTCT 1268
 DB 182 AAAATATGAATGCTTGGGAGATTCATTTTTCATATATATTTCTTTGTTTCT 241
 QY 1269 TGTACATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1328
 DB 242 TGTACATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 301
 QY 1329 TTTACATGCAATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1388
 DB 302 TTTACATGCAATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 361
 QY 1389 GAATGTACATCTAGAGAACATTTGCCAAAGGCTTAAGCAGGCAAGAAATTAACAC 1448

Db 362 GAATGTCATCTTAAAGAACTTTGCAAGGCTTAAAGGCAAGGAAATTAACAC 421
 Qy 1449 AGAATTAATAAATAAGATTAATCTAGCTTAAATCTATACCTCTTCAAGATCCCA 1508
 Db 442 AGAATTAATAAATAAGATTAATCTAGCTTAAATCTATACCTCTTCAAGATCCCA 481
 Qy 1509 ACCAATAGGATCTGAGAAATGCTGCTTCAAAATGACTTTCACAGAGAAATTAAT 1568
 Db 482 ACCAATAGGATCTGAGAAATGCTGCTTCAAAATGACTTTCACAGAGAAATTAAT 541
 Qy 1569 TTTTCCTGCACTAGCACTTAAAGGAGATTTGAGATTAAGCTTGAAGAGTAC 1528
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 Qy 1629 ATTTCACATGATTAAGAAAGTTGACACACTGCTTGAAGTTTCAACAGATTTGACC 1688
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 Qy 1689 CTGTTTCTCTATTTTCTTATCAACCTTTTAAATAGGCAAGATTTATAGTAC 1748
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 Qy 1749 CCTCATTTAGCATGAGAAATTTGATGTTGAGTGGGATCAGTAAATTAATGGGCTCA 1808
 Db 722 CCTCATTTAGCATGAGAAATTTGATGTTGAGTGGGATCAGTAAATTAATGGGCTCA 781
 Qy 1809 TACAAGTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1868
 Db 782 TACAAGTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 839
 Qy 1869 AACTGTTAGAGACCAACAGGGTATGGGTTAGAGATTTCCAGAGCTTACATTTTCTA 1928
 Db 840 AACTGTTAGAGACCAACAGGGTATGGGTTAGAGATTTCCAGAGCTTACATTTTCTA 899
 Qy 1929 GAGGAGATTTAATTTCTTCTCACTCATCGAGTTGATTTAGAAATTTCTGAGAAC 1988
 Db 900 GAGGAGATTTAATTTCTTCTCACTCATCGAGTTGATTTAGAAATTTCTGAGAAC 959
 Qy 1989 AGAATCTAGGCTTAAATCCACTAGCTATGCTTATGCTGCTGCTGCTGCTGCTGCT 2048
 Db 960 AGAATCTAGGCTTAAATCCACTAGCTATGCTTATGCTGCTGCTGCTGCTGCTGCT 1019
 Qy 2049 CCTGCTCTTGAAGAAATGATTTCTAGCTTCACTTATTAAGATTTCTTATTCAGAA 2108
 Db 1020 CCTGCTCTTGAAGAAATGATTTCTAGCTTCACTTATTAAGATTTCTTATTCAGAA 1079
 Qy 2109 GTCTGATAGGCTTATAGCAAGTATTTATTTAAAGTCCATAGGATTTCTGATA 2168
 Db 1080 GTCTGATAGGCTTATAGCAAGTATTTATTTAAAGTCCATAGGATTTCTGATA 1139
 Qy 2169 GGCAGTGAAGTTAGGAGCCACAGTTATGAATGGAAGTATGGAATGGCAGGCTTGAAG 2228
 Db 1140 GGCAGTGAAGTTAGGAGCCACAGTTATGAATGGAAGTATGGAATGGCAGGCTTGAAG 1199
 Qy 2229 ATAACATTTGCTTTTGAATGATCTGCTAGCTGGAAGAGGAGATCTTCAAGACAT 2288
 Db 1200 ATAACATTTGCTTTTGAATGATCTGCTAGCTGGAAGAGGAGATCTTCAAGACAT 1259
 Qy 2289 GCTTTATTTGGGCTTTTGTGAGATGAAGCAAGGACTTTGAGACCAAGAAACCAATCTG 2348
 Db 1260 GCTTTATTTGGGCTTTTGTGAGATGAAGCAAGGACTTTGAGACCAAGAAACCAATCTG 1319
 Qy 2349 ACTTAGGATGAGAAATGAGCAATTTTGTCTGAGAGGCTATTAACAGAGGTTATAGG 2408
 Db 1320 ACTTAGGATGAGAAATGAGCAATTTTGTCTGAGAGGCTATTAACAGAGGTTATAGG 1379
 Qy 2409 TTTTATTTTCAACAGATTAAGCAACAGTGTAAACAGAACTCAATTTACAAATATCTA 2468
 Db 1380 TTTTATTTTCAACAGATTAAGCAACAGTGTAAACAGAACTCAATTTACAAATATCTA 1439
 Qy 2469 AAACATGATCATATATGTTAGTTCAATTTCTTTTCAATCTCAGGTTCCCTCA 2528

Db 1440 AAACATGATCATATATGTTAGTTCAATTTCTTTTCAATCTCAGGTTCCCTCA 1499
 Qy 2529 TATGATTTCTTAAACATGCTTTGATCCCTTTTGAATGATATCATATTTGAAATGC 2588
 Db 1500 TATGATTTCTTAAACATGCTTTGATCCCTTTTGAATGATATCATATTTGAAATGC 1559
 Qy 2589 CTATTTATATCTTGAATTTTGTGCTGAGACTGTAAGCCATGAGGACCTTTATTTG 2648
 Db 1560 CTATTTATATCTTGAATTTTGTGCTGAGACTGTAAGCCATGAGGACCTTTATTTG 1619
 Qy 2649 AATGATCTCTGTCATCATATGATGCTCTTTGCTCATCATTTGATCCCTGAGAAATG 2708
 Db 1620 AATGATCTCTGTCATCATATGATGCTCTTTGCTCATCATTTGATCCCTGAGAAATG 1679
 Qy 2709 GCTTAGAATTAATAGTGTATAGCTTGAACACCGGTTATTTTCAACACCTGATCT 2768
 Db 1680 GCTTAGAATTAATAGTGTATAGCTTGAACACCGGTTATTTTCAACACCTGATCT 1739
 Qy 2769 TCTGCTGGAACATATAGCAAGGCAATTTTCAAGCTTCTTGAATGAGTATTTAA 2828
 Db 1740 TCTGCTGGAACATATAGCAAGGCAATTTTCAAGCTTCTTGAATGAGTATTTAA 1799
 Qy 2829 TTTGAGCATTAATCTTCAATGATGATGAGATGATGATGATGATGATGATGATGAT 2888
 Db 1800 TTTGAGCATTAATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1859
 Qy 2889 TAAACCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2948
 Db 1860 TAAACCTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1919
 Qy 2949 GTTACACAGATTAATCAACAGAGCTGATTTCTGAAAAAATGTCAGAGCCAAAC 3008
 Db 1920 GTTACACAGATTAATCAACAGAGCTGATTTCTGAAAAAATGTCAGAGCCAAAC 1979
 Qy 3009 TCTGCTATTTGCAATCTTCACTTATTTGATGAGAGGATTTGATGATGATGATGAT 3068
 Db 1980 TCTGCTATTTGCAATCTTCACTTATTTGATGAGAGGATTTGATGATGATGATGAT 2039
 Qy 3069 GTACTATTTGTCAAG 3084
 Db 2040 GTACTATTTGTCAAG 2055

RESULT 10
 US-10-144-678A-917
 ; Sequence 917, Application US/10144678A
 ; Publication No. US20030157089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jianshun
 ; APPLICANT: Dillon, Devin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Ranger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yashir A. W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Hurst, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals y de Bassole, Carlota
 ; APPLICANT: Foy, Teresa M.
 ; APPLICANT: Matanabe, Yoshihiro
 ; APPLICANT: Deng, Ta
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND


```

1  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
2
3  FILE REFERENCE:  210121.427C28
4
5  CURRENT APPLICATION NUMBER:  US/10/144,678A
6
7  CURRENT FILING DATE:  2003-08-12
8
9  NUMBER OF SEQ. ID NOS.:  1033
10
11  SOFTWARE:  FASTSEQ for Windows Version 3.0
12
13  SEQ. ID NO. 917
14
15  LENGTH:  2061
16
17  TYPE:  DNA
18
19  ORGANISM:  Homo sapiens
20
21  US-10-144-678A-917

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Query Match	64.7%	Score 2028.4	DB 13	Length 2061
Best Local Similarity	99.8%	Pred. No. 0		
Matches 2052	Conservative	0	Mismatches	1
			Indels	3
			Gaps	2

QY	1023	GAATGACACAGGCGCATCTTCACATCTTTCACATGTCGACACACAGCTTCAGACCCCTAGT	1088
Dp	3	GAATGACACAGGCGCATCTTCACATCTTTCACATGTCGACACACAGCTTCAGACCCCTAGT	62
QY	1089	GTCCAGTGCATCAACTTCTTTCACATTCAGAGTCTCTGATTCAGATTTTAATGTTAACAT	1148
Dp	63	GTCCAGTGCATCAACTTCTTTCACATTCAGAGTCTCTGATTCAGATTTTAATGTTAACAT	122
QY	1149	TTTGGAGACAGATATTCAGAAAAAAATTCCTTAATPAATAAATCACTCAGATCTCTC	1208
Dp	123	TTTGGAGACAGATATTCAGAAAAAAATTCCTTAAT -AAAAATCACTCAGATCTCTC	181
QY	1209	AAATATGAAACTGCTGGTGGGGAACTCCATTTTTCAAATATTAATTTCTTCTTGTTCCT	1268
Dp	182	AAATATGAAACTGCTGGTGGGGAACTCCATTTTTCAAATATTAATTTCTTCTTGTTCCT	241
QY	1269	TGCTACATATTAATTTAATACCTCGACTAGTGTGGTGGAGGGTTATTAATCTTTTCAT	1328
Dp	242	TGCTACATATTAATTTAATACCTCGACTAGTGTGGTGGAGGGTTATTAATCTTTTCAT	301
QY	1329	TTTACACATGAGATCCAAATCTTAACTGCTCTACTAGTGGTTTACAGACTTCAGATPA	1388
Dp	302	TTTACACATGAGATCCAAATCTTAACTGCTCTACTAGTGGTTTACAGACTTCAGATPA	361
QY	1389	GAATGGTACATCTAGAGAACATTTGCCAAAGGCGCTAAGCAGCGCAAGGAAATTAACAC	1448
Dp	362	GAATGGTACATCTAGAGAACATTTGCCAAAGGCGCTAAGCAGCGCAAGGAAATTAACAC	421
QY	1449	AAATATTAATTAATAGATATCTACTTAAACTTAACTTAACTTCTTTCAGAACTCCCA	1508
Dp	422	AAATATTAATTAATAGATATCTACTTAAACTTAACTTAACTTCTTTCAGAACTCCCA	481
QY	1509	ACCACATTTGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAATAT	1568
Dp	482	ACCACATTTGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAATAT	541
QY	1569	TTTTCTCTGACACTAGCACTTAAAGGGGAAGTTGGAAGTAAAGCTTTGAAGAAGTAC	1628
Dp	542	TTTTCTCTGACACTAGCACTTAAAGGGGAAGTTGGAAGTAAAGCTTTGAAGAAGTAC	601
QY	1629	ATTTACCTACGTTATGAAAAGTTGACACATGTTCTGAGAGTTTTCACACGATATGAGCC	1688
Dp	602	ATTTACCTACGTTATGAAAAGTTGACACATGTTCTGAGAGTTTTCACACGATATGAGCC	661
QY	1689	CTGTTTTCTCATTAAATTTTCTTATCAACCTTTAATTTAGGCAAGATATTAATTAAGTAC	1748
Dp	662	CTGTTTTCTCATTAAATTTTCTTATCAACCTTTAATTTAGGCAAGATATTAATTAAGTAC	721
QY	1749	CCTCATTTAGCCATGGGAAAATTTGATGTTCACTGGGGAATCAGTGAATTTAAATGGGCTCA	1808
Dp	722	CCTCATTTAGCCATGGGAAAATTTGATGTTCACTGGGGAATCAGTGAATTTAAATGGGCTCA	781
QY	1809	TACAGATTAATAATTTAAAAAAAGCTTCATGCCCATCTCATATGATGTGGAGG	1868
Dp	782	TACAGATTAATAATTT -AAAAAAAGAGCTTCATGCCCATCTCATATGATGTGGAGG	839
QY	1869	AACTGTTAGAGAGCAACAGGGTATGAGGTTAGAGATTTCCAGAGCTTTCATATTTCTA	1928

Db	840	AACGTTAGAGAGCAACAGGTAAGTGGATTAGAGATTTCAGAGCTTACATTCTTA	899
Qy	1929	GAGAGGTAATTAAATTTCTTCACTACCAAGATGTGATTTAGAAATTTCTGGCAAC	1988
Db	900	GAGAGGTAATTAAATTTCTTCACTACCAAGATGTGATTTAGAAATTTCTGGCAAC	959
Qy	1989	AGAACTCAAGGTTAATCCCACTAGCAATGTGATTTGTCCTGATCCAAATGGCAATTA	204
Db	960	AGAACTCAAGGTTAATCCCACTAGCAATGTGATTTGTCCTGATCCAAATGGCAATTA	1015
Qy	2049	CCTGTGCTTGAAAGAAAGTGAATTTCTAGGTTCAACCATTAATGAAATTTATTCAGAA	2108
Db	1020	CCTGTGCTTGAAAGAAAGTGAATTTCTAGGTTCAACCATTAATGAAATTTATTCAGAA	1079
Qy	2109	GTCGCAATAGGCTTATAGCAAGTTATTTATTTAAAGTTCCATAGGTGATTTGATA	2166
Db	1080	GTCGCAATAGGCTTATAGCAAGTTATTTATTTAAAGTTCCATAGGTGATTTGATA	1139
Qy	2169	GGCAGTAGAGTTAGGGAGCCACAGTTATGATGGGAAGTATGAAATGGCAGGCTTTAAG	2222
Db	1140	GGCAGTAGAGTTAGGGAGCCACAGTTATGATGGGAAGTATGAAATGGCAGGCTTTAAG	1199
Qy	2229	ATPAACATTTGCCCTTTTGATGTGACTGCTAGCTGAAAGTAGGGAATCTTCAGACCAT	2288
Db	1200	ATPAACATTTGCCCTTTTGATGTGACTGCTAGCTGAAAGTAGGGAATCTTCAGACCAT	125
Qy	2289	GCTTATTTGGGGCTTTGTGCAAGTATGGAAGAGGAATTGAGACCGAAGAACTG	234
Db	1260	GCTTATTTGGGGCTTTGTGCAAGTATGGAAGAGGAATTGAGACCGAAGAACTG	1311
Qy	2349	ACTTAGGATGGGAATCAGCAATTTTGTCTTGAGGGGCTATTACCAAGGTTAATAG	2408
Db	1320	ACTTAGGATGGGAATCAGCAATTTTGTCTTGAGGGGCTATTACCAAGGTTAATAG	1379
Qy	2409	TTTCAATCTTCAACAGGATATGACAACAGTGTAAACAAAGAACTCAATTAACAATACTA	2466
Db	1380	TTTCAATCTTCAACAGGATATGACAACAGTGTAAACAAAGAACTCAATTAACAATACTA	1439
Qy	2469	AAACATGATCATATATATGTGTAAAGTTCAATTTCTTTTCANCTCAGGTTCCCTGA	2528
Db	1440	AAACATGATCATATATATGTGTAAAGTTCAATTTCTTTTCANCTCAGGTTCCCTGA	1499
Qy	2529	TATGATTTCTATAAACATGCTTTCATCCCTTTTGTAATGGAATCATATTTGAAATGC	2588
Db	1500	TATGATTTCTATAAACATGCTTTCATCCCTTTTGTAATGGAATCATATTTGAAATGC	1559
Qy	2589	CTATTTAATCTGTATTTGCTGTGACCTGTAAGCCCAAGAGGCACTGTTTATATG	2648
Db	1560	CTATTTAATCTGTATTTGCTGTGACCTGTAAGCCCAAGAGGCACTGTTTATATG	1619
Qy	2649	AATGTCAATCTGTTCATCATATGACTGCTCTCTTGTCAATCATATGAAATCCCAACAAGT	2708
Db	1620	AATGTCAATCTGTTCATCATATGACTGCTCTCTTGTCAATCATATGAAATCCCAACAAGT	1679
Qy	2709	GCCTAGAACAATATATGTCTTATGCTTGAACAACGGTATTTTTCATCAACCTGATTCCT	2768
Db	1680	GCCTAGAACAATATATGTCTTATGCTTGAACAACGGTATTTTTCATCAACCTGATTCCT	1739
Qy	2769	TCTGTCTGGAACATATAGCAGGCAATTTTTCAGGCTTGTGAGTGGGATTAATATAA	2828
Db	1740	TCTGTCTGGAACATATAGCAGGCAATTTTTCAGGCTTGTGAGTGGGATTAATATAA	1799
Qy	2829	TTCTGGCAATTTCTGCAATGTGATGGAAGTGAATGTGCAATTTCTATACCTGGCTCA	2888
Db	1800	TTCTGGCAATTTCTGCAATGTGATGGAAGTGAATGTGCAATTTCTATACCTGGCTCA	1859
Qy	2889	TAAACCTCCCAATGTGCAAGCTTTCAATGTGAATTAATATGACTTGGGAACCTATGT	2948
Db	1860	TAAACCTCCCAATGTGCAAGCTTTCAATGTGAATTAATATGACTTGGGAACCTATGT	1919
Qy	2949	GTTACACAGATTAATCACACAGAGCCTGTGATTTCTGAAAATACTGTGACAGACCAAC	3008

Db 1920 GTTACACAGATTAATCACCAGAACCTGATTTCTGAAAAAACTGTCAGAGCCAAACC 1979
QY 3009 TCTGTCATTTGGCACTCCCACTTGTATTTGTACGAGGAGGTTGATTAAGTAAATAA 3068
Db 1980 TCTGTCATTTGGCACTCCCACTTGTATTTGTACGAGGAGGTTGATTAAGTAAATAA 2039
QY 3069 GTACTATTTGTGTCAG 3084
Db 2040 GTACTATTTGTGTCAG 2055

RESULT 11
US-10-294-025-917
; Sequence 917, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; NUMBER OF FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 917
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-917

Query Match 64.7%; Score 2028.4; DB 13; Length 2061;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 1029 GATTGACAGGCGCATCTTCGACTTTTCATGTGCGCCACAGCCCTCAGAGCCCTAGGT 1088
Db 3 GATTGACAGGCGCATCTTCGACTTTTCATGTGCGCCACAGCCCTCAGAGCCCTAGGT 62
QY 1089 GTGCTGATTCAACTCTTTTCCATTCAGAGTCTCTGATTCAGATTTTAATGTTAAAT 1148
Db 63 GTGCTGATTCAACTCTTTTCCATTCAGAGTCTCTGATTCAGATTTTAATGTTAAAT 122
QY 1149 TTTGGAGACAGTATTCAGAAAAAAATTTCTTAAATAAATAACAGTCAATCTTC 1208
Db 123 TTTGGAGACAGTATTCAGAAAAAAATTTCTTAAATAAATAACAGTCAATCTTC 181
QY 1209 AAATATGAACCTGTTGGGGAATCTCCATTTTTCATTAATTAATTTCTTTGTTTCT 1268
Db 182 AAATATGAACCTGTTGGGGAATCTCCATTTTTCATTAATTAATTTCTTTGTTTCT 241
QY 1269 TGCTACATATTAATTAATACCTGACTAGTGTGTTGGAGGGTTATTAATCTTTTCA 1328
Db 242 TGCTACATATTAATTAATACCTGACTAGTGTGTTGGAGGGTTATTAATCTTTTCA 301
QY 1329 TTTACCATGACGTCCTAAATCTGTTCTACTGATGTTTACAGACATCTGAGATTA 1388
Db 302 TTTACCATGACGTCCTAAATCTGTTCTACTGATGTTTACAGACATCTGAGATTA 361
QY 1389 GAATGTCATCTAGAGAACTTTGGCAAGGCTTAAGCAAGGAAAGAAATAAATC 1448
Db 362 GAATGTCATCTAGAGAACTTTGGCAAGGCTTAAGCAAGGAAAGAAATAAATC 421
QY 1449 AGAATATTAATAATGAGATTAATCTAGCTTAATACTTAATCTTCTGAGAACTCCA 1508
Db 422 AGAATATTAATAATGAGATTAATCTAGCTTAATACTTAATCTTCTGAGAACTCCA 481
QY 1509 ACCCATATGATCTCAGAAAAATGCTGTTCAAAAAGACTCTTACAGAGAAATAAAT 1568
Db 482 ACCCATATGATCTCAGAAAAATGCTGTTCAAAAAGACTCTTACAGAGAAATAAAT 541
QY 1569 TTTCTCTGACACTAGCACTTAAGGGGAAGATTGAGTAAGCCTTGAAAGAGTAC 1628

Db 542 TTTTCTCTGACACTAGCACTTAAGGGGAAGATTGAAAGTAAAGCTTGAAAGATAC 601
QY 1629 ATTACCTAGATTAATGAAAGTTGACACCTGTTCTGAGAGTTTTCACAGATATGACC 1688
Db 602 ATTACCTAGATTAATGAAAGTTGACACCTGTTCTGAGAGTTTTCACAGATATGACC 661
QY 1689 CTGTTTCTCTGATTAATTTTCTGATCAACCTTTAATTAAGGCAAGATTAATTAATGTC 1748
Db 662 CTGTTTCTCTGATTAATTTTCTGATCAACCTTTAATTAAGGCAAGATTAATTAATGTC 721
QY 1749 CCTCATTTGAGCCATGAGAAAAATGATGTCAGTGGGATCAAGTAATTAATGAGGTCA 1808
Db 722 CCTCATTTGAGCCATGAGAAAAATGATGTCAGTGGGATCAAGTAATTAATGAGGTCA 781
QY 1809 TACAATATTAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1868
Db 782 TACAATATTAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 839
QY 1869 AACTGTTAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 1928
Db 840 AACTGTTAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 899
QY 1929 GAGAGGATTTTAATTTCTTCACTCACTCACTGTTGATTTAGAAATTTCTGCAAC 1988
Db 900 GAGAGGATTTTAATTTCTTCACTCACTCACTGTTGATTTAGAAATTTCTGCAAC 959
QY 1989 AGAAGTATGAGCTTAATCCCACTAGCTATGCTTAATGCTGTTGCAATGCAATTA 2048
Db 960 AGAAGTATGAGCTTAATCCCACTAGCTATGCTTAATGCTGTTGCAATGCAATTA 1019
QY 2049 CCTGTCCTTGGAAAGAGTATTTCTAGGTTCAACATTAAGAAATTTCTTACAGAA 2108
Db 1020 CCTGTCCTTGGAAAGAGTATTTCTAGGTTCAACATTAAGAAATTTCTTACAGAA 1079
QY 2109 GTCTGATAGGCTTTATGAGTAATTTTAAAGTCCATAGTGTATGTTGTA 2168
Db 1080 GTCTGATAGGCTTTATGAGTAATTTTAAAGTCCATAGTGTATGTTGTA 1139
QY 2169 GGCAGTGAAGTTAGGAGCAACAGTATGATGGAAGTGAAGTGAAGCTTGAAG 2228
Db 1140 GGCAGTGAAGTTAGGAGCAACAGTATGATGGAAGTGAAGTGAAGCTTGAAG 1199
QY 2229 ATTAATGAGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2288
Db 1200 ATTAATGAGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1259
QY 2289 GCTTAATTTGGGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2348
Db 1260 GCTTAATTTGGGCTTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1319
QY 2349 ACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2408
Db 1320 ACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1379
QY 2409 TTTCACTTTCACACAGATATGACACAGTGTAAACCAAGAACTCAATTAATACTA 2468
Db 1380 TTTCACTTTCACACAGATATGACACAGTGTAAACCAAGAACTCAATTAATACTA 1439
QY 2469 AAACATGATATATATGATGTAAGTTCAATTTCTTTTCAATCTGAGGTTCCCTGA 2528
Db 1440 AAACATGATATATATGATGTAAGTTCAATTTCTTTTCAATCTGAGGTTCCCTGA 1499
QY 2529 TATGATTTCTTAATAACATGCTTCAATCCCTTTGTAATGATATCAATTTGGAATGTC 2588
Db 1500 TATGATTTCTTAATAACATGCTTCAATCCCTTTGTAATGATATCAATTTGGAATGTC 1559
QY 2589 CTATTTATATCTGATTTGCTGCTGAGCTGAAGCCATGAGGCACTGTTATTAATG 2648
Db 1560 CTATTTATATCTGATTTGCTGCTGAGCTGAAGCCATGAGGCACTGTTATTAATG 1619
QY 2649 AATGTCATCTGCTCATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2708

Db 1620 AATCTCATCTCTGTTTCATTCATTCAGTCTCTTTCATCATTCAGTAATCCCCAGCAAGT 1679
 QY 2709 GCGTAGAACAATATAGTCTTATGCTTACAGCCGGTATTTTCATCAAACTGATTCTT 2768
 Db 1680 GCGTAGAACAATATAGTCTTATGCTTACAGCCGGTATTTTCATCAAACTGATTCTT 1739
 QY 2769 TCTGCTCTGAACACATAGCCAGGCAATTTTCAGCTCTCTTGAAGTGGTATTATTA 2828
 Db 1740 TCTGCTCTGAACACATAGCCAGGCAATTTTCAGCTCTCTTGAAGTGGTATTATTA 1799
 QY 2829 TTCTGCGCATTAATCTTCCATGTAGTGAAGTGAATGCAATTTCTATACCTGAGCTA 2888
 Db 1800 TTCTGCGCATTAATCTTCCATGTAGTGAAGTGAATGCAATTTCTATACCTGAGCTA 1859
 QY 2889 TAAACCTCTCCATGTCAGCTCTTTCATGTGTAATTAATGTGACTTGGGAAGCTATGT 2948
 Db 1860 TAAACCTCTCCATGTCAGCTCTTTCATGTGTAATTAATGTGACTTGGGAAGCTATGT 1919
 QY 2949 GTTACAGAGATTAATACAGAGAAAGCTGATTTCTGAAAACCTGCGAGCCAAAC 3008
 Db 1920 GTTACAGAGATTAATACAGAGAAAGCTGATTTCTGAAAACCTGCGAGCCAAAC 1979
 QY 3009 TCTGTCTTGTGCACTCCCACTTGTATTTGTACAGAGCACTTGATTAAGTGAATAATA 3068
 Db 1980 TCTGTCTTGTGCACTCCCACTTGTATTTGTACAGAGCACTTGATTAAGTGAATAATA 2039
 QY 3069 GTACTATTGTCTCAAG 3084
 Db 2040 GTACTATTGTCTCAAG 2055

RESULT 12

US-10-012-896-917
 : Sequence 917, Application US/10012896
 : Publication No. US20020183251A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, Davin C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Kalos, Michael D.
 : APPLICANT: Reiter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvick, Thomas S.
 : APPLICANT: Carter, Derrick
 : APPLICANT: Li, Samuel X.
 : APPLICANT: Wang, Aijun
 : APPLICANT: Skeiky, Yasir A.W.
 : APPLICANT: Hepler, William T.
 : APPLICANT: Henderson, Robert A.
 : APPLICANT: Hural, John
 : APPLICANT: McNeill, Patricia D.
 : APPLICANT: Houghton, Raymond L.
 : APPLICANT: Vitale de Bassols, Carolea
 : APPLICANT: Roy, Teresa
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Mantanabe, Yoshihiro
 : APPLICANT: Meagher, Madeleine Joy
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 : FILE REFERENCE: 210121.427C27
 : CURRENT APPLICATION NUMBER: US/10/012, 896
 : NUMBER OF SEQ ID NOS: 1011
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 917
 : LENGTH: 2061
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-10-012-896-917

Query Match 64.7%; Score 2028.4; DB 14; Length 2061;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
 QY 1029 GATTGACAGAGGACCTCTTGACATTTTCATGTGGCCACACAGGCTTCAGAGCCCTAGGT 1088
 Db 3 GATTGACAGAGGACCTCTTGACATTTTCATGTGGCCACACAGGCTTCAGAGCCCTAGGT 62
 QY 1089 GTGAGTATCAAACTCTTTCCATGAGTCCCTGATTCAGATTCTTAATGTTAATACAT 1148
 Db 63 GTGAGTATCAAACTCTTTCCATGAGTCCCTGATTCAGATTCTTAATGTTAATACAT 122
 QY 1149 TTGGAGACAGTATTCAGAAAAAATTTCTTAATTAATAAATACACTGAGATCTCTTC 1208
 Db 123 TTGGAGACAGTATTCAGAAAAAATTTCTTAATTAATAAATACACTGAGATCTCTTC 181
 QY 1209 AAATATGAACTGGTGGGGAATCCATTTTTCATTAATATTTCTGCTGTTTCTT 1268
 Db 182 AAATATGAACTGGTGGGGAATCCATTTTTCATTAATATTTCTGCTGTTTCTT 241
 QY 1269 TGTACATATAATTAATTAATACCTGATAGTGTGGTGGAGGTATTACTTTTCAT 1328
 Db 242 TGTACATATAATTAATTAATACCTGATAGTGTGGTGGAGGTATTACTTTTCAT 301
 QY 1329 TTTACATGACGTCCCAATCTTAACTGCTTCTACTGATGTTTACAGATTTCTGAGTTA 1388
 Db 302 TTTACATGACGTCCCAATCTTAACTGCTTCTACTGATGTTTACAGATTTCTGAGTTA 361
 QY 1389 GAATGTACATCTGAGAAACCTTGCAGAAAGGCTTAAGCAGGCAAGAAATAACAC 1448
 Db 362 GAATGTACATCTGAGAAACCTTGCAGAAAGGCTTAAGCAGGCAAGAAATAACAC 421
 QY 1449 AGAATATATAATTAATGATTAATCTAGCTTAAACCTTAATCTTTTGAACCTCCCA 1508
 Db 422 AGAATATATAATTAATGATTAATCTAGCTTAAACCTTAATCTTTTGAACCTCCCA 481
 QY 1509 ACCCATGTGATCTCAGAAAAATGCTGCTTCAAAAAGACTTCAAGAGAGAAATAAT 1568
 Db 482 ACCCATGTGATCTCAGAAAAATGCTGCTTCAAAAAGACTTCAAGAGAGAAATAAT 541
 QY 1569 TTTTCTCTGACACTAGCACTTAAGGGAAGATTTGGAAGTAAAGCTTGAAGAGTAC 1628
 Db 542 TTTTCTCTGACACTAGCACTTAAGGGAAGATTTGGAAGTAAAGCTTGAAGAGTAC 601
 QY 1629 ATTTACCTAGCTTAATAAAGTTCAGCACTGTTCTGAGAGTTTTCACAGATATGAGAC 1688
 Db 602 ATTTACCTAGCTTAATAAAGTTCAGCACTGTTCTGAGAGTTTTCACAGATATGAGAC 661
 QY 1689 CTGTTTTTCTATTTAATTTCTATCAACCTTTAATTAGGCAAGATATTATTAGTAC 1748
 Db 662 CTGTTTTTCTATTTAATTTCTATCAACCTTTAATTAGGCAAGATATTATTAGTAC 721
 QY 1749 CCTATGTTGACCATGGGAAATTTGATGTTCACTGGGATCACTGAATTAATGGGGTCA 1808
 Db 722 CCTATGTTGACCATGGGAAATTTGATGTTCACTGGGATCACTGAATTAATGGGGTCA 781
 QY 1809 TACAAGTATATAATTAATAAAGAGCTTCATGCCCATCTCATATGATGTGAGAG 1868
 Db 782 TACAAGTATATAATTAATAAAGAGCTTCATGCCCATCTCATATGATGTGAGAG 839
 QY 1869 AACTGTTAGAGACCAAGGAGTGTAGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 1928
 Db 840 AACTGTTAGAGACCAAGGAGTGTAGGTTAGAGATTTCCAGAGTCTTACATTTTCTA 899
 QY 1929 GAGGAGTATTTAATTTCTCTCACTCATCAAGTGTGTTTAGAATTTCTGCGAAC 1988
 Db 900 GAGGAGTATTTAATTTCTCTCACTCATCAAGTGTGTTTAGAATTTCTGCGAAC 959
 QY 1989 AGAATCATAGCTTAATTCCTCACTAGCTATGCTTATGCTGTCGAATTCGAATTA 2048
 Db 960 AGAATCATAGCTTAATTCCTCACTAGCTATGCTTATGCTGTCGAATTCGAATTA 1019
 QY 2049 CCGTGTCTTGAAGAAAGTATTTCTAGGTTACCAATTAAGAAAGTCTTATTCAGAAA 2108

Db 1020 CCGTGGTCTGGAGAGAGATTCTAGGTCACCAATTATGGAACATCTTATTCAGAAA 1079
Qy 2109 GTCTGCATAGGGCTTATAGCAAGTATTTATTTAAAGTTCATAGAGTCTGATA 2168
Db 1080 GTCTGCATAGGGCTTATAGCAAGTATTTATTTAAAGTTCATAGAGTCTGATA 1139
Qy 2165 GGCAGTGAAGTTAGGAGCCACCAAGTATGATGAGGAAGTATGGAATGGCAGGCTTGAAG 2228
Db 1140 GGCAGTGAAGTTAGGAGCCACCAAGTATGATGAGGAAGTATGGAATGGCAGGCTTGAAG 1199
Qy 2229 ATAACTATGAGCTTTGAGTGAAGTCTGAGTGAAGGAAGTGAAGGAATCTCAGAGCAT 2288
Db 1200 ATAACTATGAGCTTTGAGTGAAGTCTGAGTGAAGGAAGTGAAGGAATCTCAGAGCAT 1259
Qy 2289 GCTTTATTTGGGCTTTGTGCAAGTATGGAACAGGACTTTGAGACAGGAAGCAATCTG 2348
Db 1260 GCTTTATTTGGGCTTTGTGCAAGTATGGAACAGGACTTTGAGACAGGAAGCAATCTG 1319
Qy 2349 ACTTAGGAGATGGGAATCAGGCAATTTTGTCTGTGAGGGGCTTATACCAAGGCTTATAGG 2408
Db 1320 ACTTAGGAGATGGGAATCAGGCAATTTTGTCTGTGAGGGGCTTATACCAAGGCTTATAGG 1379
Qy 2409 TTTCACTTTCAACAGAGATATGCAACAGTGTATACCAAGAACTCAATTAACAATACTA 2468
Db 1380 TTTCACTTTCAACAGAGATATGCAACAGTGTATACCAAGAACTCAATTAACAATACTA 1439
Qy 2469 AAACATGATATCATATATGTGTAGTTCATTTCTTTTCAATCTCAGGTTCCCTGA 2528
Db 1440 AAACATGATATCATATATGTGTAGTTCATTTCTTTTCAATCTCAGGTTCCCTGA 1499
Qy 2529 TATGATTCCTATTAACATGCTTTTCAATCCCTTTTGAATGGAATGATATTTGGAATGC 2588
Db 1500 TATGATTCCTATTAACATGCTTTTCAATCCCTTTTGAATGGAATGATATTTGGAATGC 1559
Qy 2589 CTATTTATATCTTGTATTTTGTCTGTGAGTGAAGCCCATAGGCACTGTTATTTATTTG 2648
Db 1560 CTATTTATATCTTGTATTTTGTCTGTGAGTGAAGCCCATAGGCACTGTTATTTATTTG 1619
Qy 2649 AATGTCATCTGTGTCATCATATGAGTGTCTTTGTCTGATCAATGAATCCCCAGCAAGT 2708
Db 1620 AATGTCATCTGTGTCATCATATGAGTGTCTTTGTCTGATCAATGAATCCCCAGCAAGT 1679
Qy 2709 GCTTAGAACAATATATGTGTATGCTTAGACACCGGTTATTTTTCATCAAACTGATTCCT 2768
Db 1680 GCTTAGAACAATATATGTGTATGCTTAGACACCGGTTATTTTTCATCAAACTGATTCCT 1739
Qy 2769 TCTGTCCGAACAATATGAGTGTATGCTTAGACACCGGTTATTTTTCATCAAACTGATTCCT 2828
Db 1740 TCTGTCCGAACAATATGAGTGTATGCTTAGACACCGGTTATTTTTCATCAAACTGATTCCT 1799
Qy 2829 TTTGAGCATTACTTCCAAATGTAGTGAAGTGAATGATGCAATTTCTAATCTGAGCTCA 2888
Db 1800 TTTGAGCATTACTTCCAAATGTAGTGAAGTGAATGATGCAATTTCTAATCTGAGCTCA 1859
Qy 2889 TAAACCCCTCCCAAGTGAAGGCTTTCAATGTTGAATTAATGTAATCTTGGAGACTATGT 2948
Db 1860 TAAACCCCTCCCAAGTGAAGGCTTTCAATGTTGAATTAATGTAATCTTGGAGACTATGT 1919
Qy 2949 GTTACACAGAGTAATCAACAGAGGCTTGAATTTCTGAAAAAACTGTGACAGGCAAAACC 3008
Db 1920 GTTACACAGAGTAATCAACAGAGGCTTGAATTTCTGAAAAAACTGTGACAGGCAAAACC 1979
Qy 3009 TCTGTCAATTTGCAATCCCACTTGTATTTGTACAGAGGAGTGTGATTAAGTGAATAATATA 3068
Db 1980 TCTGTCAATTTGCAATCCCACTTGTATTTGTACAGAGGAGTGTGATTAAGTGAATAATATA 2039
Qy 3069 GTACTATTTGTCAAG 3084
Db 2040 GTACTATTTGTCAAG 2055

RESULT 13

US-09-366-459A-4
; Sequence 4, Application US/0966459A
; Publication No. US2003002237A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J.N.
; APPLICANT: MINTER, G.
; APPLICANT: RAMANATHAN, C.S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M.G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HEPREMY4,
; FILE OF INVENTION: EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG
; FILE REFERENCE: D0039NP
; CURRENT APPLICATION NUMBER: US/09/966,459A
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,833
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,776
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/305,351
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,202
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-966-459A-4
Query Match 63.5%; Score 1992.6; DB 11; Length 2034;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 4; Indels 4; Gaps 3;
Qy 1087 GTGTGAGTATCAAACTTCTTCCATTCAGAGTCTCGATTGAGATTTATGTATAC 1146
Db 1 GTGTGAGTATCAAACTTCTTCCATTCAGAGTCTCGATTGAGATTTATGTATAC 60
Qy 1147 ATTTTGAAGACAGTATTCAGAAAAAATTTCTTAATTAATAATCACTCAGATCT 1206
Db 61 ATTTTGAAGACAGTATTCAGAAAAAATTTCTTAAT -AAAAATACAACTCAGATCT 119
Qy 1207 TCAAAATATGAACGTGTTGGGAATCTCAATTTTCAATATATTTCTTTGTTT 1266
Db 120 TCAAAATATGAACGTGTTGGGAATCTCAATTTTCAATATATTTCTTTGTTT 179
Qy 1267 CTGTGCAATATATTAATTAATACCTGAGTATGAGTGTGAGGAGTTATTAATCTTTC 1326
Db 180 CTGTGCAATATTAATTAATTAATACCTGAGTATGAGTGTGAGGAGTTATTAATCTTTC 239
Qy 1327 ATTTTACATGAGTCCAAATCTAATGCTTCTAATGATGTTTACAGCAATCTGAGAT 1386
Db 240 ATTTTACATGAGTCCAAATCTAATGCTTCTAATGATGTTTACAGCAATCTGAGAT 299
Qy 1387 AAGAAATGATCATCTAGAGAACTTTGCAAAAGGCTTAGACAAGGCAAGAAAAATAAC 1446
Db 300 AAGAAATGATCATCTAGAGAACTTTGCAAAAGGCTTAGACAAGGCAAGAAAAATAAC 359
Qy 1447 ACAGAAATTAATAAATAGATTAATCTGCTTAAATCTAATCTCTTCAAGAACTCC 1506
Db 360 ACAGAAATTAATAAATAGATTAATCTGCTTAAATCTAATCTCTTCAAGAACTCC 419
Qy 1507 CAACCAATGTGATCTCAGAAAAATGCTGTCTTCAAAAATGAATTTCTACAGAGAAATA 1566
Db 420 CAACCAATGTGATCTCAGAAAAATGCTGTCTTCAAAAATGAATTTCTACAGAGAAATA 479
Qy 1567 ATTTTCCCTGGAGACATGACCTTAAGGGAAGATTTGAGTAAAGCTTGAAGAGCT 1626
Db 480 ATTTTCCCTGGAGACATGACCTTAAGGGAAGATTTGAGTAAAGCTTGAAGAGCT 539
Qy 1627 ACATTTACTACGTTAATGAAGTTGACACACTGTCTGAGAGTTTTCACAGCATATGGA 1686

Db 540 ACAATTACACGTAATGAAAGTGAACAACCTCTGAGATTTCACAGCATAGGA 599
Qy 1887 CCCCTGTTTCCATTTATTTCTTATCAACCCCTTATATAGCAAGATATTAAT 1746
Db 600 CCCGTTTTCCTATTTATTTCTTATCAACCCCTTATATAGCAAGATATTAAT 659
Qy 1747 ACCCTCATTTGAGCATGGGAAATTTGATGTCAGTGGGATCACTGAATTAATGGG 1806
Db 660 ACCCTCATTTGAGCATGGGAAATTTGATGTCAGTGGGATCACTGAATTAATGGG 719
Qy 1807 CATACAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1866
Db 720 CATACAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 777
Qy 1867 AGAAGCTGTAGAGACCAACAGGGTATGGGTTAGAGATTTCCAGAGTTCATTTTC 1926
Db 778 AGAAGCTGTAGAGACCAACAGGGTATGGGTTAGAGATTTCCAGAGTTCATTTTC 837
Qy 1927 TAGAGAGATATTTATTTCTTCACTC-ATCCAGTGTATTAATTAAGAAATTTCTGGC 1985
Db 838 TAGAGAGATATTTATTTCTTCACTCCTCCAGTGTATTAATTAAGAAATTTCTGGC 897
Qy 1986 AACGAACTCATGGCTTTAATCCCATAGCTATTTGCTTATTTCTGATTCATTCGCA 2045
Db 898 AACGAACTCATGGCTTTAATCCCATAGCTATTTGCTTATTTCTGATTCATTCGCA 957
Qy 2046 TTACCTGTCTTGGAGAGATTTCTAGTGTACCTGATTCACATATAGAAAGATTTATTCG 2105
Db 958 TTACCTGTCTTGGAGAGATTTCTAGTGTACCTGATTCACATATAGAAAGATTTATTCG 1017
Qy 2106 AAAGCTGATAGGGCTTATAGCAAGTATTTATTTTAAAGTTCATAGGTATTCG 2165
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Db 1078 ATAGGAGTGAAGTTAGGAGCCACCACTTATATGAGAAATATGGAATGGCAGTCTTG 1137
Qy 2226 AAGTAACATTTGGCTTTTGAAGTGTACCTGATTCGAAAGGAGGAAATCTTCAGAGC 2285
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Db 1198 CATGCTTATTTGGGCTTTTGTACATATGAAACAGGACCTTTGAGACCCAGGAAAGCAT 1257
Qy 2346 CTGACTTAGGCAATGAGCAATTTTGTCTTGAAGGGCTATTTACCAAGGTTAAT 2405
Db 1258 CTGACTTAGGCAATGAGCAATTTTGTCTTGAAGGGCTATTTACCAAGGTTAAT 1317
Qy 2406 AGGTTTCATTTCAACAGATATGACACAGAGTATTAACCAAGAACTCAATTAACAATA 2465
Db 1318 AGGTTTCATTTCAACAGATATGACACAGAGTATTAACCAAGAACTCAATTAACAATA 1377
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Db 1378 CTAAACATGTATCTATATATGTGTAAGTTTCATTTCTTTCAATCTCAAGTTCC 1437
Qy 2526 TGATATGATTTCTATATACATGTTTCATCCCTTTGTAATGATATCATATTTGGAAA 2585
Db 1438 TGATATGATTTCTATATACATGTTTCATCCCTTTGTAATGATATCATATTTGGAAA 1497
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Qy 2646 TTGAATGTATCTGTATCATTTGATGCTTGTGATCATATGAAATCCCCAGAGAA 2705
Db 1558 TTGAATGTATCTGTATCATTTGATGCTTGTGATCATATGAAATCCCCAGAGAA 1617
Qy 2706 AGTGCTTAAGCAATAATAGTGTATGCTTGAACCCGTTATTTTCAATCAACCTGAT 2765

Db 1618 AGTGCTTAAGCAATAATAGTGTATGCTTGAACCCGTTATTTTCAATCAACCTGAT 1677
Qy 2766 CCTTCTGTCCGAAACACATAGCAGCAATTTTCAGCTTCTTGAATGGTATTAAT 2825
Db 1678 CCTTCTGTCCGAAACACATAGCAGCAATTTTCAGCTTCTTGAATGGTATTAAT 1737
Qy 2826 AAATTCGCGCAATTAATTCATATGATGAGTGAAGTGAATTCATATTAATCTGGC 2885
Db 1738 AAATTCGCGCAATTAATTCATATGATGAGTGAAGTGAATTCATATTAATCTGGC 1797
Qy 2886 TCATTAACCCCTCCATGATGAGCTTTCATGTTGATCACTTAATGATCTTGGAAAGTA 2945
Db 1798 TCATTAACCCCTCCATGATGAGCTTTCATGTTGATCACTTAATGATCTTGGAAAGTA 1857
Qy 2946 TGTGTACAGAGATTAATCAACAGAAAGCTGATTTCTGAAAAAAGCTGACAGCCAA 3005
Db 1858 TGTGTACAGAGATTAATCAACAGAAAGCTGATTTCTGAAAAAAGCTGACAGCCAA 1917
Qy 3006 ACCCTGTCAATTTGCAATCCCACTTGTATTTGTACAGAGCAATTTGATTAAGTAAAT 3065
Db 1918 ACCCTGTCAATTTGCAATCCCACTTGTATTTGTACAGAGCAATTTGATTAAGTAAAT 1977
Qy 3066 AAAGTACTATTTGTCAAGAAAAAATTAATTAATTAATTAATTAATTAATTAAT 3122
Db 1978 AAAGTACTATTTGTCAAGAAAAAATTAATTAATTAATTAATTAATTAATTAAT 2034

RESULT 14
US-09-759-143-916
; Sequence 916, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu JIANGCHUN
; APPLICANT: Dillon, Devin C.
; APPLICANT: Hitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Panger, Gary R.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yaser A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 916
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-916

Query Match 41.1%; Score 1287.8; DB 9; Length 1302;
Best Local Similarity 99.8%; Pred. No. 3.9e-303;
Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 52 TGACAAAGGGGGTCAACATTTCTTCCATAGCGTTGAGCTTACTGCTGCTGCTG 111
Db 1 TGACAAAGGGGGTCAACATTTCTTCCATAGCGTTGAGCTTACTGCTGCTGCTG 60
Qy 112 TCACAGTTAGCTTCTTCATGATGATGATCCCAATGGCAGATGATCCAGTCTACATAC 171
Db 61 TCACAGTTAGCTTCTTCATGATGATGATCCCAATGGCAGATGATCCAGTCTACATAC 120

QY 172 TTTCATCTTAATAGGCTCCCTGGTTTAAAGAGCTCACTTCTGGTTGGCCCTTCCCATG 231
Db 121 TTTCATCTTAATAGGCTCCCTGGTTTAAAGAGCTCACTTCTGGTTGGCCCTTCCCATG 180
QY 232 TGTCCCTCTACCTTAATAGGCTAGGTAATGACATCATGATGAGGCT 291
Db 181 TGTCCCTCTACCTTAATAGGCTAGGTAATGACATCATGATGAGGCT 240
QY 292 GAGCAGAGCTGATAGGCTCAATGATATATTTCTTGGATGCTTTCAGGATGACATC 351
Db 241 GAGCAGAGCTGATAGGCTCAATGATATATTTCTTGGATGCTTTCAGGATGACATC 300
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Db 301 CTCATCTCCAGCTCAATGACATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 360
QY 412 ATCCAGTTTGAATGCTTGTCTGCTAAGATTTTGGCATTCACCTTATCTGGATGGA 471
Db 361 ATCCAGTTTGAATGCTTGTCTGCTAAGATTTTGGCATTCACCTTATCTGGATGGA 420
QY 472 TCACAGTGTCTGCTGCTGCTGCTTTCACCTTATGAGGCTATGCTACCTGCTGCTGCT 531
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QY 532 CATGCAAGTATCTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 591
Db 481 CATGCAAGTATCTTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 592 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 651
Db 541 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 652 AATATCTCTTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
Db 601 AATATCTCTTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 712 ATCCGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 771
Db 661 ATCCGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 772 CTTCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 831
Db 721 CTTCATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 832 GCCCAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
Db 781 GCCCAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 892 GTACCTTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
Db 841 GTACCTTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
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Db 901 CCCGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
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Db 1021 GCTTCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1132 GATTTTATGTTTACATTTGGAAGACATGATGAGAAAAATTTCTTAAATTAATAA 1191
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QY 1192 TACAACTCAGATCTTCAATATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1251
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QY 1252 TTTCCTCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
Db 1200 TTTCCTCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259
QY 1312 GGGTATTAATTTTCAATTTTACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
Db 1260 GGGTATTAATTTTCAATTTTACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302

RESULT 15
US-09-780-669-916
Sequence 916, Application US/09780669
Patent No. US2002005197A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780, 669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 916
LENGTH: 1302
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-916

Query Match 41.1%; Score 1287.8; DB 9; Length 1302;
Best Local Similarity 99.8%; Pred. No. 3.9e-303;
Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 52 TGAGCAAGGGGCTGACATCTCTCCATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 111
Db 1 TGAGCAAGGGGCTGACATCTCTCCATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 60
QY 112 TCACAGTTCAGCTTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 171
Db 61 TCACAGTTCAGCTTCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 172 TTTCATCTTAATAGGCTCCCTGGTTTAAAGAGCTCACTTCTGGTTGGCCCTTCCCATG 231
Db 121 TTTCATCTTAATAGGCTCCCTGGTTTAAAGAGCTCACTTCTGGTTGGCCCTTCCCATG 180
QY 232 TGTCCCTCTACCTTAATAGGCTAGGTAATGACATCATGATGAGGCT 291
Db 181 TGTCCCTCTACCTTAATAGGCTAGGTAATGACATCATGATGAGGCT 240
QY 292 GAGCAGAGCTGATAGGCTCAATGATATATTTCTTGGATGCTTTCAGGATGACATC 351
Db 241 GAGCAGAGCTGATAGGCTCAATGATATATTTCTTGGATGCTTTCAGGATGACATC 300
QY 352 CTCATCTCCAGCTCAATGACATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 411

Db 301 CTCATCTCCACCTCATCCAGTCCCAAAATGCTGGCACTCTTGTGTTCAATTCACCTACC 360
 QY 412 ATCCAGTTTGTGCTTGTCTGTCTACAGATTTTGGCATTCACCTCCTTATCTGGCATGAA 471
 Db 361 ATCCAGTTTGTGCTTGTCTGTCTACAGATTTTGGCATTCACCTCCTTATCTGGCATGAA 420
 QY 472 TCCACAGTGTCTGTGGCCATGGCTTTTGGACCGCTATGTGGCCATCTGTACCCCATGGCC 531
 Db 421 TCCACAGTGTCTGTGGCCATGGCTTTTGGACCGCTATGTGGCCATCTGTACCCCATGGCC 480
 QY 532 CATGCCACAGTACTTACGTTGCTCGTGTACCAAAATGGTGGCTGTGTGGCGG 591
 Db 481 CATGCCACAGTACTTACGTTGCTCGTGTACCAAAATGGTGGCTGTGTGGCGG 540
 QY 592 GGGGCTGCACTGATGGCACTCCCTTCTGTCTCATCAAGCACTGCCCTTCTGCGCTCC 651
 Db 541 GGGGCTGCACTGATGGCACTCCCTTCTGTCTCATCAAGCACTGCCCTTCTGCGCTCC 600
 QY 652 AATATCCTTCCCATCTGCTACCTGCTACACCAAGATGTCAAGAGCTGGCTGTGTAT 711
 Db 601 AATATCCTTCCCATCTGCTACCTGCTACACCAAGATGTCAAGAGCTGGCTGTGTAT 660
 QY 712 ATCCGGGTCAATGTCTATGTGCTTATGTGATCATCTCCGCTATGGCTGTGACTCA 771
 Db 661 ATCCGGGTCAATGTCTATGTGCTTATGTGATCATCTCCGCTATGGCTGTGACTCA 720
 QY 772 CTTCCTATCTCTCTCTCTATATCTGTCTTATCTTAAAGCTGTGTGGCTTGAACCTGAA 831
 Db 721 CTTCCTATCTCTCTCTCTATATCTGTCTTATCTTAAAGCTGTGTGGCTTGAACCTGAA 780
 QY 832 GCCCAGGCCAAGGCATTTGGCACTGTGGCTCTCATGTGTGTGTGTGTGTATCTAT 891
 Db 781 GCCCAGGCCAAGGCATTTGGCACTGTGGCTCTCATGTGTGTGTGTGTGTATCTAT 840
 QY 892 GTACCTTCTATGTGATTTGTCCATGTGCATGCTGTTAGCAAGCGGCTGACTCTCGCTG 951
 Db 841 GTACCTTCTATGTGATTTGTCCATGTGCATGCTGTTAGCAAGCGGCTGACTCTCGCTG 900
 QY 952 CCGGTCACTGTGGCAATATCTATCTGTGTCTCTGCTGTCAACCCATTTGTCTAT 1011
 Db 901 CCGGTCACTGTGGCAATATCTATCTGTGTCTCTGCTGTCAACCCATTTGTCTAT 960
 QY 1012 GAGGTGAAGCAAAAGAGATTCGACGCGATCTTCGACTTTTCCATGTGGCCACACAC 1071
 Db 961 GAGGTGAAGCAAAAGAGATTCGACGCGATCTTCGACTTTTCCATGTGGCCACACAC 1020
 QY 1072 GCTTCAGAGCCCTAGGTGTGAGTATCAAACTCTTTCCATTCAGAGTCTCTGATTCA 1131
 Db 1021 GCTTCAGAGCCCTAGGTGTGAGTATCAAACTCTTTCCATTCAGAGTCTCTGATTCA 1080
 QY 1132 GATTTTAATGTAACTTTTGGAAAGACAGTATTCAGAAAAAAATTTCTTATATAAAA 1191
 Db 1081 GATTTTAATGTAACTTTTGGAAAGACAGTATTCAGAAAAAAATTTCTTATATAAAA 1135
 QY 1192 TAAACTCAGATCTCTCAATATGAAGTGTGTGGGAAATTCOACTTTTCAATATTAT 1251
 Db 1140 TAAACTCAGATCTCTCAATATGAAGTGTGTGGGAAATTCOACTTTTCAATATTAT 1199
 QY 1252 TTTCTCTTTGTTTCTGTCTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 1311
 Db 1200 TTTCTCTTTGTTTCTGTCTACATTAATTAATTAATTAATTAATTAATTAATTAATTA 1259
 QY 1312 GGGTTTAACTTTTCAATTTTACCATGAGTCCAAATCTAAACT 1354
 Db 1260 GGGTTTAACTTTTCAATTTTACCATGAGTCCAAATCTAAACT 1302

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 16:05:18 / Search time 6213 Seconds
(without alignments)
1267.638 Million cell updates/sec

Title: US-10-017-066a-1

Perfect score: 1 cagagagcgctgtatcagc.....aaaaaaaaaaaaaaaa 3136

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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17: em_gse_hum:*
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19: em_gse_pin:*
20: em_gse_vrt:*
21: em_gse_fun:*
22: em_gse_mam:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rnd:*
26: em_gse_png:*
27: em_gse_vrt:*
28: gb_gse1:*
29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	701	22.4	702	13	EX092732	EX092732
2	684.8	21.8	753	9	AU138663	AU138663
3	606.8	19.3	765	28	AF101565	AF101565
4	568.6	18.1	664	10	BF679294	BF679294

5	547.8	17.5	779	10	BG541042	BG541042
6	544.6	17.4	559	9	AF694767	AF694767
7	519.4	15.6	862	10	BF674120	BF674120
8	498.4	15.0	505	9	AF1871596	AF1871596
9	471.8	15.0	483	9	AF138131	AF138131
10	464.4	14.8	466	9	AF771398	AF771398
11	444.6	14.2	660	10	BG653241	BG653241
12	443	14.1	448	9	AA988520	AA988520
13	442	14.1	445	10	BE550795	BE550795
14	442	14.1	447	9	AF631017	AF631017
15	441	14.1	450	10	BF433082	BF433082
16	440	14.0	443	9	AF145747	AF145747
17	432.2	13.8	632	10	BB665936	BB665936
18	400.2	12.8	705	9	AF106391	AF106391
19	399.4	12.7	507	14	CD286823	CD286823
20	398.4	12.7	400	13	BX283988	BX283988
21	379.4	12.1	454	9	AU157695	AU157695
22	378	12.1	386	9	AA531196	AA531196
23	355	11.3	1964	11	AK036356	AK036356
24	355	11.3	3410	11	AK028467	AK028467
25	343.8	11.0	353	9	AA622418	AA622418
26	336.4	10.7	338	10	BG212555	BG212555
27	302.4	9.6	583	4	BX525010	BX525010
28	284.2	9.1	1086	28	AF101706	AF101706
29	281.8	9.0	296	9	AA689245	AA689245
30	280	8.9	447	9	AM235635	AM235635
31	274.2	8.7	795	29	BZ256668	BZ256668
32	260.4	8.3	662	10	BB550626	BB550626
33	254	8.1	462	10	BF002049	BF002049
34	246.2	7.9	301	9	AM078525	AM078525
35	202.2	6.4	565	10	AM962764	AM962764
36	200.4	6.4	773	28	BH112117	BH112117
37	199.4	6.4	695	28	BH043372	BH043372
38	194.8	6.2	820	28	BH046083	BH046083
39	191.4	6.1	705	28	AF101881	AF101881
40	187.8	6.0	798	28	BZ612040	BZ612040
41	187.8	6.0	821	28	BZ195145	BZ195145
42	184.2	5.9	798	28	BH082934	BH082934
43	181.4	5.8	588	28	AZ006959	AZ006959
44	176.6	5.6	859	28	BZ221157	BZ221157
45	176	5.6	784	29	BZ248123	BZ248123

ALIGNMENTS

RESULT 1
EX092732

LOCUS
DEFINITION
IMAGE:1602508, mRNA sequence.

ACCESSION
EX092732

VERSION
EX092732.1 GI:27825459

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 702)
Ebert L., Heil O., Hennig S., Neubert P., Partsch E., Peters M., Radelof V., Schneider D. and Korn B.
Human Unigeneset - RZPD3

TITLE
JOURNAL
Unpublished

COMMENT
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IMAGP981054063
RZPDLB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLB No. 972)
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi?response?libNo=972
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany

Db 302 TTACATGACGATCCAAATCTTAACGTCTTACTGATGTTTACAGCATTCGAGATTA 361
 QY 1389 GAATGATGATCTTGAAGAACTTTGCCAAGGCTTAAGCAGCGAAAGAAAATAACAC 1448
 Db 362 GAATGATGATCTTGAAGAACTTTGCCAAGGCTTAAGCAGCGAAAGAAAATAACAC 421
 QY 1449 AGAATATATATTAATGAGATATCTAGTCTTAAATCTTAATCTTCTTGAAGATCCCA 1508
 Db 422 AGAATATATATTAATGAGATATCTAGTCTTAAATCTTAACTTCTTGAAGATCCCA 481
 QY 1509 ACCACATGATGATCTGAGAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAAATAAT 1568
 Db 482 ACCACATGATGATCTGAGAAAATGCTGTCTTCAAAATGACTTCTACAGAGAAAATAAT 541
 QY 1569 TTTTCTCTGAGACCTGACCTTAAAGGGGAAAGTTGG-AGTAAAGCTTGAAGAGTA 1627
 Db 542 TTTTCTCTGAGACCTGACCTTAAAGGGGAAAGTTGG-AGTAAAGCTTGAAGAGTA 601
 QY 1628 CATTTACTAGTATGATGAGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGAC 1687
 Db 602 CATTTACTAGTATGATGAGAAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGAC 661
 QY 1688 CCTGTCTTCTGATTTATTTCTTCTTCAACCTTTAATTAATTAAGCAA--AGATATTTATTA 1744
 Db 662 CCTGTCTTCTGATTTATTTCTTCTTCAACCTTTAATTAATTAATTAAGCAA--AGATATTTATTA 721
 QY 1745 GTACCTCATGTTAGCAGCATGGGAAA 1770
 Db 722 GTACCTCATGTTAGCAGCATGGGAAA 747

RESULT 3
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 LOCUS AF101565 Human Homo sapiens genomic clone PAC298B117end, genomic
 DEFINITION survey sequence.
 ACCESSION AF101565
 VERSION AF101565.1 GI:4193525
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 765)
 AUTHORS Bepler, G., O'Brian, K.C., Kim, Y.C., Schreiber, G., and Pitterle, D.M.
 TITLE A 1.4-Mb high-resolution physical map and contig of chromosome
 segment 11p15.5 and genes in the LOH1A metastasis suppressor
 region
 JOURNAL Genomics 55 (2), 164-175 (1999)
 MEDLINE 99134294
 PUBMED 9933563
 COMMENT Contact: Bepler G
 Medicine and Radiology
 Duke University Medical Center
 Box 2610, MSRB, Room 117, Durham, NC 27710, USA
 part of a 1.4 megabase contig including the LOH1A metastasis
 suppressor region
 Class: unknown.
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 /clone_1b="Human"
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 Best Local Similarity 98.9%; Pred. No. 3.5e-54;
 Matches 611; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2477 GATCATATATGATGATGATTTTCTTTTCTTCAATCTGAGGTTCCCTGATATGATTT 2536
 Db 1 GATCATATATGATGATGATTTTCTTTTCTTCAATCTGAGGTTCCCTGATATGATTT 60
 QY 2537 CCTATTAACATGATTTTCAATCTTCTTTTGAATGATATCATATTTGAAATGCTATTTAA 2596
 Db 61 CCTATTAACATGATTTTCAATCTTCTTTTGAATGATATCATATTTGAAATGCTATTTAA 120
 QY 2597 TACTGTATTTGCTGCTGAGACCTGTAAGCCCATGAGGACATGTTATTAATGAATGAT 2656
 Db 121 TACTGTATTTGCTGCTGAGACCTGTAAGCCCATGAGGACATGTTATTAATGAATGAT 180
 QY 2657 CTCTGTATCATGATGATGCTGCTTCTTCTGATCATATTAATCCCAAGAAATGCTTAA 2716
 Db 181 CTCTGTATCATGATGATGCTGCTTCTTCTGATCATATTAATCCCAAGAAATGCTTAA 240
 QY 2717 CATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2776
 Db 241 CATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 2777 GAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2836
 Db 301 GAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 2837 ATTACTTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2896
 Db 361 ATTACTTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 QY 2897 TCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2956
 Db 421 TCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 2957 GAGTAAATCACAAGAGGCTGATTTCTGAAAAAATCTGCGAGGCCAACTCTGTGAT 3016
 Db 481 GAGTAAATCACAAGAGGCTGATTTCTGAAAAAATCTGCGAGGCCAACTCTGTGAT 540
 QY 3017 TTGCAATCTCCACCTGTATTTGTACGAGGAGTGTGATGATGATGATGATGATGATGAT 3076
 Db 541 TTGCAATCTCCACCTGTATTTGTACGAGGAGTGTGATGATGATGATGATGATGATGAT 600
 QY 3077 GTGTCAAGTCTGTGAAA 3094
 Db 601 GTGTCAAGTCTGTGAAA 618

RESULT 4
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 LOCUS BE679294 602153488F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294532 5',
 DEFINITION mRNA sequence.
 ACCESSION BE679294
 VERSION BE679294.1 GI:11953189
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 664)
 AUTHORS NIH-MGC
 TITLE NIH-MGC
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: gsabds-rc@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
 http://image.llnl.gov
 Plate: LCM1143 row: P column: 21
 High quality sequence stop: 601.
 Location/Qualifiers

source

1..664

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4294532"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH MGC 83"

/note="Organ: Prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcggc); Site 2: SfiI (ggccatcggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 137 a 187 c 147 g 193 t

ORIGIN

Query Match 18.1%; Score 568.6; DB 10; Length 664;
Best Local Similarity 99.0%; Pred. No. 3.5e-50;
Matches 593; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

43 GAGGAGAGCTGACAAAGGGGCTCAACATTCCTTCATACGCTTGAAGCTCTACCTGCC 102
1 GAGGAGAGCTGACAAAGGGGCTCAACATTCCTTCATACGCTTGAAGCTCTACCTGCC 60
103 TGGTCTGTGACATTCAGCTTCTTCAATGATGGATGCCAATGGCAATGAATCCAGT 162
61 TGGTCTGTGACATTCAGCTTCTTCAATGATGGATGCCAATGGCAATGAATCCAGT 120
163 GCTACATCTTCATCTCAATAGGCTCCCTGGTTAGAAAGAGCTCAGTTCTGGTGGCC 222
121 GCTACATCTTCATCTCAATAGGCTCCCTGGTTAGAAAGAGCTCAGTTCTGGTGGCC 180
223 TTCCATCTGTGCTCCTCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 282
181 TTCCATCTGTGCTCCTCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 240
283 GTGGGAGCTGAGCAGAGCTCATGAGGCCCATGATATATTTCTTTCAGATCTTTCAGC 342
241 GTGGGAGCTGAGCAGAGCTCATGAGGCCCATGATATATTTCTTTCAGATCTTTCAGC 300
343 ATTGACATCTTCATCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 402
301 ATTGACATCTTCATCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 360
403 TTCCATCTGTGCTCCTCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 462
361 TTCCATCTGTGCTCCTCTCACTTATGCTGTGCTAGGTAATTGACATCATCTACAT 420
463 GGACATGATCAACAGTCTGCTGAGCCATGCTTTTACCGCTATGAGCATCTGTAC 522
421 GGACATGATCAACAGTCTGCTGAGCCATGCTTTTACCGCTATGAGCATCTGTAC 479
523 CCACGCGCCCATGACAGTACTTACGTTGCTGTGTACCAAAATGTTGTGTGCTGCT 582
480 CCACGCGCCCATGACAGTACTTACGTTGCTGTGTACCAAAATGTTGTGTGCTGCT 539
583 GTGGTGGCGGGGCTGCACTGATGG-CACCCCTTCTGTCTTCAATCAAGAGAGCTGCC 640
540 GTGGTGGCGGGGCTGCACTGATGGCAACCCCTTCTGTCTTCAATCAAGAGAGCTGCC 598

RESULT 5
BS541042 779 bp rRNA linear EST 03-APR-2001
LOCUS 602570205F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694856 5'
DEFINITION
RNA sequence.
ACCESSION
BS541042
VERSION
BS541042.1 GI:13533275
KEYWORDS
EST.

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 779)

NIH-MGC <http://mgs.nci.nih.gov/>, National Institutes of Health, Mammalian Gene Collection (MGC)

UNPUBLISHED

Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Plate: LLCM1519 row: 1 column: 01

FEATURES

source

Location/Qualifiers

1..779

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4694856"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcggc); Site 2: SfiI (ggccatcggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC library."

BASE COUNT 145 a 205 c 198 g 231 t

ORIGIN

Query Match 17.5%; Score 547.8; DB 10; Length 779;
Best Local Similarity 91.8%; Pred. No. 4.5e-48;
Matches 614; Conservative 0; Mismatches 47; Indels 8; Gaps 3;

1 CAGAGAGCTGATTCAGTGAGGCTGCAAGCTCTTGGAGAGAGCTGCAAG 60
17 CAGAGAGCTGATTCAGTGAGGCTGCAAGCTCTTGGAGAGAGCTGCAAG 76
61 GGGGTCAACATTCCTTCATACGGTTGAGCTTACCTGCTGCTGTGCAAGTT 120
77 GGGGTCAACATTCCTTCATACGGTTGAGCTTACCTGCTGCTGTGCAAGTT 136
121 AGCTCTTCATAGATGTGATGCCAATGGCAATGAATGATGCTACATCTTATCTTA 180
137 AGCTCTTCATAGATGTGATGCCAATGGCAATGAATGATGCTACATCTTATCTTA 196
181 ATAGAGCTCCCTGTTTGAAGAGGCTCAAGTTGTTGGCTTCCATTGGCTCCCTC 240
197 ATAGAGCTCCCTGTTTGAAGAGGCTCAAGTTGTTGGCTTCCATTGGCTCCCTC 256
241 TACCTTATGCTGTGCTAGTAACTTGAATCAATCAATTTGCGGAGCTGAGCAGC 300
257 TACCTTATGCTGTGCTAGTAACTTGAATCAATCAATTTGCGGAGCTGAGCAGC 316
301 CTGATGAGCCCATGATATATTTCTTTCAGAGCTTTCAGGATGACATCTCATCTCC 360
317 CTGATGAGCCCATGATATATTTCTTTCAGAGCTTTCAGGATGACATCTCATCTCC 376
361 ACCTTATCAAGCCCAAAATGCTGCGCAATCTTGTGTTCAATTCACTACATCAAGTT 420
377 ACCTTATCAAGCCCAAAATGCTGCGCAATCTTGTGTTCAATTCACTACATCAAGTT 436
421 GATGCTGTGCTAGTAAAGATTTTTCATCAGTCACTCTTATCTGAGAGGATTCAGAGT 480

Db	437	GAGGCTTGCTGTGTACAGATGGTTGGCATTCCACTCTTATCTTGGCATGGAAATCACAGTG	496
QY	481	CTGCTGGCCATGGCTTTTATGACGGATATGGCATCTGTGCACCCACTGGCGCATGGACCA	540
Db	497	CTGCTGGCCATGGCTTTTATGACGGATATGGCATCTGTGCACCCACTGGCGCATGGACCA	555
QY	541	GTACTTA-GCTTGCCCTCTGTACCAAAA-----TTGCTGTGCTCTGTGTGCGGGG	593
Db	556	GTACTTAACGTTGCTCTGTGTGTTCACAAAATGGTGTGGGTGCTGTGTGTGGGGGGGG	615
QY	594	GGGTGCATGATGGCAACCCCTTCCTGTCTTATCATCAGCAGGTGACCTTTGTCCGCTTCAA	653
Db	616	GCTGAGCTGGTGGAGACCCCTTTCCTGTCTTTCATTAAGGACATGGCTTTTGGGGCTTAAT	675
QY	654	TATCCTTTC	662
Db	676	TTCCCTTTC	684

RESULT	6
LOCUS	A1694767/c
DEFINITION	wA1694767 559 bp mRNA EST-18-DEC-1998
ACCSSION	M1694767
VERSION	A1694767
KEYWORDS	mRNA sequence.
SOURCE	A1694767.1 GI:4382667
ORGANISM	Homo sapiens (human)
TITLE	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 559) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished Contact: Robert Strausberg, Ph.D.

JOURNAL
COMMENT
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgsab-rs@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA library preparation: M. Bento Soares, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
www.bio.lnlnl.gov/bbrp/image/image.html
Insert length: 661 Std Error: 0.00
Seq primer: -400P from Gldco
High quality sequence stop: 417.
Location/Qualifiers
1..559
source

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FEATURES
source
1..559
location/Qualifiers
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/note="Organ: lung; Vector: pUT3D-pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI CGAP Lu5 was prepared, and 35 circles were used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 141920-141791 and 1520904-152239). Subtraction by Bencic Soares and M. Fatima Bonardo."
ORIGIN
183 a
99 c 110 g 167 t

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	Matches	550;	Conservative	0;	Mismatches	9;	Indels	0;	Gaps	0
QY	2543	ACATGCTTTCA	TCCCCCTTTTGTATGAGATCATATTTGGAAATGCTATTTAAATACCTTG	2602						
Db	559	ACATGCTTTCA	TCCCCCTTTTGTATGAGATCATATTTGGAAATGCTATTTAAATACCTTG	500						
QY	2603	TATTTGCTGCTGGA	CTGTATAGCCCATGAGGGACAGTTTATATATGATATGTCATCTCGT	2662						
Db	499	TATTTGCTGCTGGA	CTGTATAGCCCATGAGGGACAGTTTATATGATATGTCATCTCGT	440						
QY	2663	TCATCATTTAGCTG	CTTTTGTCTCATCATTTGAATCCCCCAGAGAAAGTGCTAGACATAT	2722						
Db	439	TCATCATTTAGCTG	CTTTTGTCTCATCATTTGAATCCCCCAGAGAAAGTGCTAGACATAT	380						
QY	2723	AGTGTATTATGCTTG	ACACCCGTTATTTTTCATACAACTGATTCCTCTGTCTGACAC	2782						
Db	379	AGTGTATTATGCTTG	ACACCCGTTATTTTTCATACAACTGATTCCTCTGTCTGACAC	320						
QY	2783	ATAGCAGGCAATTTT	CCAGCCTTCTTGAATGGGTATTTATTAATCTGGGCCATTCT	2842						
Db	319	ATAGCAGGCAATTTT	CCAGCCTTCTTGAATGGGTATTTATTAATCTGGGCCATTCT	260						
QY	2843	TCCAATGTAGTGA	AGTGAATGCAATTTCTATACCTGGCTCATAAACCCCTCCAT	2902						
Db	259	TCCAATGTAGTGA	AGTGAATGCAATTTCTATACCTGGCTCATAAACCCCTCCAT	200						
QY	2903	GTGACAGCTTTCA	TGTGTACATTTAAATGTGACTGGGAAGCTATGTGTACACAGATTA	2962						
Db	199	GTGACAGCTTTCA	TGTGTGTACATTTAAATGTGACTGGGAAGCTATGTGTACACAGATTA	140						
QY	2963	ATCACCAAGAACCT	GTGAATTTCTGAATAAACTGTGCAGAGCCAAACCTGTGCATTTGCA	3022						
Db	139	ATCACCAAGAACCT	GTGAATTTCTGAATAAACTGTGCAGAGCCAAACCTTTGTGCATTTGCA	80						
QY	3023	CTCCCACTGTATT	TGTATGATACAGAGCAGTTGATTAAGTAAAAATTAAGTACTATTGTGTCA	3082						
Db	79	CTCCCACTGTATT	TGTATGATACAGAGCAGTTGATTAAGTAAAAATTAAGTACTATTGTGTCA	20						
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Site_1: SfiI (ggccgctggcc); Site_2: SfiI (ggccattggcc)
; 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAAGGCGCATTAAGCC-3' and 3' adaptor
sequence: 5'-ATCTAGAGCGCGCGGCGGACATG-3' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
BASE COUNT      185 a      233 c      223 t
ORIGIN
Query Match      16.6%; Score 519.4; DB 10; Length 862;
Best Local Similarity 97.1%; Pred. No. 3.8e-45;
Matches 603; Conservative 0; Mismatches 11; Indels 7; Gaps 7;
QY 41 TGGAGAAAGACTGACAAAGGAGGAGTCAACATTCCTTCATACGCTTGAAGCCTTACTG 100
DB 2 TGGAGAAAGACTGACAAAGGAGGAGTCAACATTCCTTCATACGCTTGAAGCCTTACTG 61
QY 101 CCTGATGCTGTCATACAGTTCATCTTTCATGATGATGATCCCAATGGCAATGATCCA 160
DB 62 CCTGATGCTGTCATACAGTTCATCTTTCATGATGATGATCCCAATGGCAATGATCCA 121
QY 161 GTGCTACATTAATCTTCTTAATAGGAGCTCCTGCTTTAGAGAGGCTCAATGCTGCTTGG 220
DB 122 GTGCTACATTAATCTTCTTAATAGGAGCTCCTGCTTTAGAGAGGCTCAATGCTGCTTGG 181
QY 221 CCTTCCCATGCTGCTCCTCTTACCTTATGCTGCTAGTACTGATCAATCAATCA 280
DB 182 CCTTCCCATGCTGCTCCTCTTACCTTATGCTGCTAGTACTGATCAATCAATCA 241
QY 281 TTGTCGGAGTACAGACAGGCTGATGAGCCATGATATATTTCTTGCATGCTTTCAG 340
DB 242 TTGTCGGAGTACAGACAGGCTGATGAGCCATGATATATTTCTTGCATGCTTTCAG 301
QY 341 GCATTTGATACCTTCATCTCCACCTCATCATGATGCCCAATGCTGGCATCTTGTGTTCA 400
DB 302 GCATTTGATACCTTCATCTCCACCTCATCATGATGCCCAATGCTGGCATCTTGTGTTCA 361
QY 401 ATTCACATACATCCAGTTT-TGATGCT-TGCTGCTCAAGAT-TTTTGCATCCACTCTT 457
DB 362 ATTCACATACATCCAGTTT-TGATGCT-TGCTGCTCAAGAT-TTTTGCATCCACTCTT 421
QY 458 TATCTGAGTGAATTCACAGTGTGCTGGCCATGGC-TTTTGAACGCTATGTCGCATC 516
DB 422 TATCTGAGTGAATTCACAGTGTGCTGGCCATGGC-TTTTGAACGCTATGTCGCATC 481
QY 517 TGTCAACCACTGGCGCATGCGACAGTACTTACGTTGCTGTGTG-CACCAAAATGGTGT 575
DB 482 TGTCAACCACTGGCGCATGCGACAGTACTTACGTTGCTGTGTG-CACCAAAATGGTGT 541
QY 576 GAGTGTGCTGTGAGGAGGAGGCTGACATGATGACACCCCTTCTCTTCAACAGAGCT 635
DB 542 GAGTGTGCTGTGAGGAGGAGGCTGACATGATGACACCCCTTCTCTTCAACAGAGCT 600
QY 636 GCCCTTTCGCGGCTCAATAT 656
DB 601 G-CCTTTCGCGGCTCAATATCT 620

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RESULT 8
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LOCUS A1871596/c
DEFINITION we28b05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342385 3',
ACCESSION A1871596

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VERSION A1871596.1 GI:5545645
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 505)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished
CONTACT: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LMW at:
www.bio.lml.gov/bdrp/image/image.html
Insert Length: 938 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
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/notes="Organ: Lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Plasmid DNA from the normalized
library NCI CGAP LUS was prepared, and as circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clones
1414920-1417951 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT      165 a      95 c      109 g      136 t
ORIGIN
Query Match      15.9%; Score 498.4; DB 9; Length 505;
Best Local Similarity 99.8%; Pred. No. 7.7e-43;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2585 ATGCTATTATTAATCTGATTTGCTGCTGAGCTGATAGCCATGAGGCACTGTTATT 2644
DB 505 ATGCTATTATTAATCTGATTTGCTGCTGAGCTGATAGCCATGAGGCACTGTTATT 446
QY 2645 ATTGAATGTCATCTGTTTCAATGATGCTCTTGTGCTCATCATTTGAATCCCCACAGA 2704
DB 445 ATTGAATGTCATCTGTTTCAATGATGCTCTTGTGCTCATCATTTGAATCCCCACAGA 386
QY 2705 AAGTGTCTAGAACATAATAGTCTATGCTGACACCGGTTATTTTCATCAAACTGAT 2764
DB 385 AAGTGTCTAGAACATAATAGTCTATGCTGACACCGGTTATTTTCATCAAACTGAT 326
QY 2765 TCCTTCTGTCTGAAACATAGACGAGCAATTTTCCAGCTTCTTTGAGTTGGGATTAAT 2824
DB 325 TCCTTCTGTCTGAAACATAGACGAGCAATTTTCCAGCTTCTTTGAGTTGGGATTAAT 266
QY 2825 TAAATTCGACCACTTCCATGATGAGTGAAGTGAATGTCATTTTCAATCTG 2884
DB 265 TAAATTCGACCACTTCCATGATGAGTGAAGTGAATGTCATTTTCAATCTG 206
QY 2885 CTCATTAACCTTCCCATGATGAGCTTTCATGTTGACATTAATGATCTGGAGACT 2944
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 DB 145 ATGTGTTACAGAGTAATACACGAGAGCTGATTTCTGAAAAAATCTGTGACAGACCA 86
 QY 3005 AACCTGTCTATTTGCAACTCCCACTTGTATTTGTACAGAGAGTTGGATTAATGAAAA 3064
 DB 85 AACCTGTCTATTTGCAACTCCCACTTGTATTTGTACAGAGAGTTGGATTAATGAAAA 26
 QY 3065 TAAAGTACTATTTGTCTCAAG 3084
 DB 25 TAAAGTACTATTTGTCTCAAG 6

RESULT 9
 AM138131/c 483 bp mRNA linear EST 29-OCT-1999
 LOCUS
 DEFINITION UI-H-B11-acy-a-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
 IMAGE:2715926 3', mRNA sequence.
 AM138131
 ACCESSION AM138131.1 GI:6142531
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 483)
 AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 COMMENT
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 The sequence contained an oligo-dt track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library preparation: W.B. Soares Lab Clone distribution:
 NCI_CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/ILNI, at:
 www.bio.illn.gov/bdrrp/image/image.html
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2715926"
 /lab_host="DH10B (Life Technologies)"
 /clone_1lb="NCI_CGAP_Sub3"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; The
 NCI_CGAP Sub3 library is a subtracted library derived from
 the NCI_CGAP Sub1 library, which is a subtracted library
 derived from B1. B1 constitutes a mixture of 21
 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
 , NCI_CGAP_Pt22, NCI_CGAP_Pt28, NCI_CGAP_Co10,
 NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
 NCI_CGAP_Kid4, NCI_CGAP_Kid11, NCI_CGAP_Kid12,
 NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_Co11, NCI_CGAP_Le12,
 NCI_CGAP_Br23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
 NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
 NCI_CGAP_Br25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below:
 NCI_CGAP_Kid3 pool 1 LLM 3334-3337, 3682-3683,
 3798-3803 (IMAGE Clonides 132376-132391, 1456008-1456775
 , 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLM 3338-3342
 , 3723-3725, 3776-3778 (IMAGE Clonides 133912-1325831,
 1471368-1472903, 1492104-1492255); NCI_CGAP_Lu5 pool 1
 LLM 3575-3582, 3851-3854 (IMAGE Clonides 1414920-1417991,
 1520904-1522439); NCI_CGAP_GC4 pool 1 LLM 3164-3167,
 3716-3720, 3733-3735 (IMAGE Clonides 1257096-1258631,

BASE COUNT 149 a 89 c 102 g 143 t
 ORIGIN
 Query Match 15.0%; Score 471.8; DB 9; Length 483;
 Best local similarity 98.6%; Pred. No. 4.5e-40;
 Matches 476; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2625 CCATGAGGCACTGTTATTTATGATGTCATCTCTGTCATCATTTGCTCTTTGCT 2684
 DB 483 CCATGAGGCACTGTTATTTATGATGTCATCTCTGTCATCATTTGCTCTTTGCT 424
 QY 2685 CATCATTAATCCGCCAGCAAGGCTCCAGCAATTAATAGCTTATGCTTGAACCGGT 2744
 DB 423 CATCATTAATCCGCCAGCAAGGCTCCAGCAATTAATAGCTTATGCTTGAACCGGT 364
 QY 2745 TATTTTTCATCAAACTGATTCCTCTGCTCCGCAACATATGACGAGCAATTTTCCAGCC 2804
 DB 363 TATTTTTCATCAAACTGATTCCTCTGCTCCGCAACATATGACGAGCAATTTTCCAGCC 304
 QY 2805 TTCTTTGAGTGGGATTAATTAATTTGCGCATTTACTTCCAAATGATGAGTGAAGTACA 2864
 DB 303 TTCTTTGAGTGGGATTAATTAATTTGCGCATTTACTTCCAAATGATGAGTGAAGTACA 244
 QY 2865 TGTGCAATTTCTAATACCTGCTCATTAACCCCTCCAGTGTGACAGCTTTGATGATCAT 2924
 DB 243 TGTGCAATTTCTAATACCTGCTCATTAACCCCTCCAGTGTGACAGCTTTGATGATCAT 184
 QY 2925 TAAATGTACCTGGGAAAGCTATGTGTACACAGATTAATACCAAGAGCTGATTTCT 2984
 DB 183 TAAATGTACCTGGGAAAGCTATGTGTACACAGATTAATACCAAGAGCTGATTTCT 124
 QY 2985 GAAAAAATCTGTGACAGCAAACTCTGTCAATTTGCACTCCCACTGATTTGTACAG 3044
 DB 123 GAAAAAATCTGTGACAGCAAACTCTGTCAATTTGCACTCCCACTGATTTGTACAG 64
 QY 3045 GCAAGTGGATTAAGTGAATAATTAAGTACTATTTGTCAAGAAAAA 3104
 DB 63 GCAAGTGGATTAAGTGAATAATTAAGTACTATTTGTCAAGAAAAA 4
 QY 3105 AAA 3107
 DB 3 AAA 1

RESULT 10
 AM771398/c 466 bp mRNA linear EST 04-MAY-2000
 LOCUS
 DEFINITION hms5907.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027612 3',
 mRNA sequence.
 AM771398
 ACCESSION AM771398.1 GI:7703453
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 466)
 AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 Unpublished

BASE COUNT 134 a 175 c 146 g 205 t
 ORIGIN

GAGAGAGATCTCCAGTTAATTAATTAATCCCCCCCCC 3,1"

Query Match 14.2% Score 444.6; DB 10; Length 660;
 Best Local Similarity 83.6%; Pred. No. 2.5e-37;
 Matches 504; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

50 ACTGAGCAAAAGGGGTCACACATCTCTCCATACAGGTTAGCCTTACCTGCTGCTGCT 109
 44 ACTGAGGGAAGAAAGACACAGAGGCTTTTCAGACAGCTGAGCTTCACTTCTGCTGCT 103
 110 GGTACAGCTTACGCTTCTTATGATGATGATCCCAATGACATGATGATGATGATGAT 169
 104 GGTACATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 163
 170 ACTTATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 229
 164 ATTTCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 223
 230 TGTGCT 289
 224 TGTGCT 283
 290 CTGAGCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 349
 284 CAGAGCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 343
 350 TCTCATCT 409
 344 TCTCATCT 403
 410 CCAATCCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
 404 CCAATCCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
 470 AATCCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
 464 AGTCCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
 530 GGCATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589
 524 GGCATGCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 583
 590 GGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
 584 GGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 643
 650 CCA 652
 644 CCA 646

RESULT 12
 AA988520 448 bp mRNA linear EST 23-JUL-1998
 LOCUS cr84803.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602508 3',
 DEFINITION mRNA sequence.

ACCESSION AA988520
 VERSION AA988520.1 GI:3174212
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 448)
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lemmon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLM at:
 www.bio.lnlnl.gov/bbtp/image/image.html
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 High quality sequence stop: 338.
 Location/Qualifiers
 1. 448
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 /clone="IMAGE:1602508"
 /issue_type="carcinoid"
 /lab_host="MDH10B"
 /clone_lib="NCI_CGAP_Lu5"
 /note="Organ: Lung; Vector: p773D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 neuroendocrine lung carcinoid, and was then primed with a
 Not I - oligo(dT) primer. Double-stranded cDNA was ligated
 to Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 p773 vector. Library is normalized. Library was
 constructed by Bento Soares and W. Fatima Boudado."

BASE COUNT 145 a 82 c 98 g 123 t
 ORIGIN

Query Match 14.1% Score 443; DB 9; Length 448;
 Best Local Similarity 100.0%; Pred. No. 4.6e-37;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2642 ATTATGAATGTCATCTGTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2701
 448 ATTATGAATGTCATCTGTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 389
 2702 GCAAGTGGCTTGAACATTAATGCTTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2761
 388 GCAAGTGGCTTGAACATTAATGCTTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 329
 2762 GATTCCTTCTGCT 2821
 328 GATTCCTTCTGCT 265
 2822 TATTAATTTCTGCGCATTAATGAT 2881
 268 TATTAATTTCTGCGCATTAATGAT 209
 2882 TGGCTCATTAACCCCTCCATGTCAGAGCTTTGAT 2941
 208 TGGCTCATTAACCCCTCCATGTCAGAGCTTTGAT 149
 2942 GCTATGTTTACACAGAGTAATACACAGAGCTGATTTGCAAAAACCTGTCAGAG 3001
 148 GCTATGTTTACACAGAGTAATACACAGAGCTGATTTGCAAAAACCTGTCAGAG 89
 3002 CCAAACTCTGTCATTTGCAACTCCCACTGTAATTTGAGAGAGAGTGGATTAAGTGA 3061
 88 CCAAACTCTGTCATTTGCAACTCCCACTGTAATTTGAGAGAGAGTGGATTAAGTGA 29
 3062 AAATTAAGTACTAATGTCAG 3084
 28 AAATTAAGTACTAATGTCAG 6

RESULT 13
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 LOCUS BE550795
 DEFINITION 759a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3232504 3',
 mRNA sequence.
 ACCESSION BE550795


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VERSION      BE550795.1  GI:9792487
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE        1 (bases 1 to 445)
JOURNAL      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              CDNA Library Preparation: M. Bento Soares, Ph.D.
              CDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/HLNLI, send email to:
              info@image.llnl.gov
              Seq primer: -400P from Gibco.
              Location/Qualifiers
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                /lab_host="DH10B"
                /clone_id="NCI CGAP Lu24"
                /note="Organ: lung; Vector: pTRT3D-Pac (Pharmacia) with a
                modified polylinker; Plasmid DNA from the normalized
                library NCI CGAP Lns was prepared, and ss circles were
                used as tracer in a subtractive hybridization reaction.
                The driver was PCR-amplified cDNAs from a pool of 5,000
                clones made from the same library (cloneids
                141920-1417991 and 1520904-1522439). Subtraction by Bento
                Soares and M. Fatima Ronaldo."
BASE COUNT   144 a      82 c      97 g      122 t
ORIGIN
Query Match      14.1%; Score 442; DB 10; Length 445;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2643 TTATTGAATGTCATCTGTCATCATTCGTCCTCTTGTGCTATCATTAATCCCCAG 2702
DB 445 TTATTGAATGTCATCTGTCATCATTCGTCCTCTTGTGCTATCATTAATCCCCAG 386
QY 2703 CAAAGTGCCTAGAACATATATAGTCTTATGCTTACACCGGTTATTTTCATCAAACTG 2762
DB 385 CAAAGTGCCTAGAACATATATAGTCTTATGCTTACACCGGTTATTTTCATCAAACTG 326
QY 2763 ATTGCTTCTGTCGACACATAGCCAGGCAATTTTCCACCTTCTTGTGCTGATTT 2822
DB 325 ATTGCTTCTGTCGACACATAGCCAGGCAATTTTCCACCTTCTTGTGCTGATTT 266
QY 2823 ATTAAATTCCTGACCATTCCTCATGTGAGTGGAATGACATGTCGAATTTCTATACCT 2882
DB 265 ATTAAATTCCTGACCATTCCTCATGTGAGTGGAATGACATGTCGAATTTCTATACCT 206
QY 2883 GGCTCATAAACCTCCCATGTCGACGCTTTCATGTTGACATTAATGTCATTTGGGAAG 2942
DB 205 GGCTCATAAACCTCCCATGTCGACGCTTTCATGTTGACATTAATGTCATTTGGGAAG 146
QY 2943 CTATGTGTTACACAGATTAATGACAGAGCCGATTTCTGAAAAAATGTCGACAGC 3002
DB 145 CTATGTGTTACACAGATTAATGACAGAGCCGATTTCTGAAAAAATGTCGACAGC 86
QY 3003 CAAAGCTCTGTGATTTGCAATCCCACTTATTTGTACAGAGCAGTTGATTAAGTAA 3062

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DB 85 CAAAGCTCTGTGATTTGCAATCCCACTTATTTGTACAGAGCAGTTGATTAAGTAA 26
QY 3063 AATTAAGTACTATTTGTGTCAG 3084
DB 25 AATTAAGTACTATTTGTGTCAG 4

RESULT 14
A1631017/c 447 bp mRNA linear EST 16-DEC-1999
LOCUS tx54el2.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273422 3'
DEFINITION mRNA sequence.
ACCESSION A1631017
VERSION A1631017.1 GI:4682347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 447)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
              Emmert-Buck, M.D., Ph.D.
              CDNA Library Preparation: M. Bento Soares, Ph.D.
              CDNA Library Arrayed by: Greg Lennon, Ph.D.
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
              found through the I.M.A.G.E. Consortium/HLNLI at:
              www.bio.llnl.gov/bbtp/image/image.html
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              Location/Qualifiers
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                modified polylinker; Plasmid DNA from the normalized
                library NCI CGAP Lns was prepared, and ss circles were
                made in vitro. Following HAP purification, this DNA was
                used as tracer in a subtractive hybridization reaction.
                The driver was PCR-amplified cDNAs from a pool of 5,000
                clones made from the same library (cloneids
                141920-1417991 and 1520904-1522439). Subtraction by Bento
                Soares and M. Fatima Ronaldo."
BASE COUNT   145 a      82 c      97 g      123 t
ORIGIN
Query Match      14.1%; Score 442; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2643 TTATTGAATGTCATCTGTCATCATTCGTCCTCTTGTGCTATCATTAATCCCCAG 2702
DB 447 TTATTGAATGTCATCTGTCATCATTCGTCCTCTTGTGCTATCATTAATCCCCAG 388
QY 2703 CAAAGTGCCTAGAACATATATAGTCTTATGCTTACACCGGTTATTTTCATCAAACTG 2762
DB 387 CAAAGTGCCTAGAACATATATAGTCTTATGCTTACACCGGTTATTTTCATCAAACTG 328
QY 2763 ATTGCTTCTGTCGACACATAGCCAGGCAATTTTCCACCTTCTTGTGCTGATTT 2822
DB 327 ATTGCTTCTGTCGACACATAGCCAGGCAATTTTCCACCTTCTTGTGCTGATTT 268

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QY 2823 ATTAATCTGGCCATTAATCTTCATGAGTGAAGTGAATGATGCAATTTCTTACT 2882
 DB 267 ATTAATCTGGCCATTAATCTTCATGAGTGAAGTGAATGATGCAATTTCTTACT 208
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 DB 207 GGGTCATTAACCCCTCCATGTCAGCCCTTCATGTCATTAATGTCAGTGGAG 148
 QY 2943 CTATGTTACACAGTAATATCAGACAGCCCTGATTTCTGAAAAAAGCTGACAGC 3002
 DB 147 CTATGTTACACAGTAATATCAGACAGCCCTGATTTCTGAAAAAAGCTGACAGC 88
 QY 3003 CAACCTCTGTCATTTGCACTCCCACTTGTATTTGTCAGAGGAGTGTAGTAA 3062
 DB 87 CAACCTCTGTCATTTGCACTCCCACTTGTATTTGTCAGAGGAGTGTAGTAA 28
 QY 3063 AATAAGTACTATTTGTGTCAAG 3084
 DB 27 AATAAGTACTATTTGTGTCAAG 6

RESULT 15

LOCUS BF433082 450 bp mRNA linear EST 29-NOV-2000
 DEFINITION 7n24f12.x1 NCI_CGAP_Lu24 Homo sapiens CDNA clone IMAGE:3565606 3',
 mRNA sequence.
 ACCESSION BF433082
 VERSION BF433082.1 GI:11445245
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 450)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapdb-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL, send email to:
info@image.lnl.gov
 Seq primer: -40UP from Gldco.

FEATURES
 source Location/Qualifiers
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 /note="Organ: lung; Vector: pT713D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI CGAP Lu5 was prepared, and as circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (cloneids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bernaldo."

BASE COUNT 144 a 83 c 98 g 125 t
 ORIGIN

Query Match 14.1%; Score 441; DB 10; Length 450;
 Best Local Similarity 100.0%; Pred. No. 7.3e-37;
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2644 TATTGATGTCATCTCTGTTCATATTGACTGCTCTTGGCTATGATGATCCCCAGC 2703
 DB 450 TATTGATGTCATCTCTGTTCATATTGACTGCTCTTGGCTATGATGATCCCCAGC 391
 QY 2704 AAGTGCCTTGAACATATATGCTTTAGCTTGAACACCGGTTATTTTCATCAAACTGA 2763
 DB 390 AAGTGCCTTGAACATATATGCTTTAGCTTGAACACCGGTTATTTTCATCAAACTGA 331
 QY 2764 TTCCTCTGCTGGAACACATAGCCAGGCAATTTTCAAGCCCTCTTGGAGTGGATTA 2823
 DB 330 TTCCTCTGCTGGAACACATAGCCAGGCAATTTTCAAGCCCTCTTGGAGTGGATTA 271
 QY 2824 TTAATTTGGCCATTTACTTCCATATGATGAGTGAAGTGAATGTCATTAACCTG 2883
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 QY 2884 GGTCAATAAACCCCTCCATGTCAGCCCTTCATGTTGACATTAATGTCATTTGGAGC 2943
 DB 210 GGTCAATAAACCCCTCCATGTCAGCCCTTCATGTTGACATTAATGTCATTTGGAGC 151
 QY 2944 TATGTTTACACAGTAATATCAGACAGACCTGATTTCTGAAAAAAGCTGACAGCC 3003
 DB 150 TATGTTTACACAGTAATATCAGACAGACCTGATTTCTGAAAAAAGCTGACAGCC 91
 QY 3004 AAACCTCTGTCATTTGCACTCCCACTTGTATTTGTCAGAGGAGTGTAGTAA 3063
 DB 90 AAACCTCTGTCATTTGCACTCCCACTTGTATTTGTCAGAGGAGTGTAGTAA 31
 QY 3064 AATAAGTACTATTTGTGTCAAG 3084
 DB 30 AATAAGTACTATTTGTGTCAAG 10

Search completed: February 9, 2004, 21:17:14
 Job time : 6223 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 16:05:17 ; Search time 1154 Seconds

(without alignments)
11501.936 Million cell updates/sec

Title: US-10-017-066a-1

Perfect score: 3136
Sequence: 1 cagagagagctgtattcagt.....aaaaaaaaaaaaaaaaaaaaa 3136

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

GenBank: 1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
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32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pln:*
35: em_hgt_rod:*
36: em_hgt_tam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3136	100.0	3136	6 AX107037	AX107037 Sequence
2	3136	100.0	3136	6 AX549148	AX549148 Sequence
3	3025.8	96.5	3077	9 HSM804438	AL833127 Homo sapi
4	2969.6	94.7	175073	2 AC105936	AC105936 Homo sapi
5	2969.6	94.7	175177	9 AC090719	AC090719 Homo sapi
6	2028.4	64.7	2061	6 AX201144	AX201144 Sequence
7	2028.4	64.7	2061	6 AX267943	AX267943 Sequence
8	2028.4	64.7	2061	6 BD160111	BD160111 Primer fo
9	2028.4	64.7	2061	9 AK023643	AK023643 Homo sapi
10	1940.8	61.9	179664	2 AC025249	AC025249 Homo sapi
11	1287.8	41.1	1302	6 AX201143	AX201143 Sequence
12	1287.8	41.1	1302	6 AX267942	AX267942 Sequence
13	1186.4	37.8	1225	9 BC022401	BC022401 Homo sapi
14	1186.2	37.8	1354	6 AX646553	AX646553 Sequence
15	1186.2	37.8	1354	9 AB065787	AB065787 Homo sapi
16	986.4	30.8	968	6 AX338395	AX338395 Sequence
17	964.2	30.7	968	6 AX338397	AX338397 Sequence
18	962.2	30.7	968	6 AX338399	AX338399 Sequence
19	955.4	30.5	957	6 AX128501	AX128501 Sequence
20	955.4	30.5	957	6 AX201145	AX201145 Sequence
21	955.4	30.5	957	6 AX267944	AX267944 Sequence
22	955.4	30.5	957	6 AX448799	AX448799 Sequence
23	955.4	30.5	957	6 BD144354	BD144354 Novel G-P
24	952.4	30.4	954	6 AX201146	AX201146 Sequence
25	952.4	30.4	954	6 AX241660	AX241660 Sequence
26	952.4	30.4	954	6 AX267945	AX267945 Sequence
27	884.2	28.2	339098	2 AC096030	AC096030 Rattus no
28	766.8	24.5	753	10 AY072993	AY072993 Mus muscu
29	684.8	21.8	427	6 BD149982	BD149982 Primer fo
30	404	12.9	437	6 AX107041	AX107041 Sequence
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32	379.4	12.1	454	6 BD154949	BD154949 Primer fo
33	379.4	12.1	945	6 AX241763	AX241763 Sequence
34	379.4	12.1	963	6 AX448797	AX448797 Sequence
35	379.4	12.1	963	6 BD144351	BD144351 Novel G-P
36	379.4	12.1	1024	6 AX551415	AX551415 Sequence
37	379.4	12.1	175073	2 AC105936	AC105936 Homo sapi
38	379.4	12.1	175177	9 AC090719	AC090719 Homo sapi
39	377.4	12.0	963	6 AR261055	AR261055 Sequence
40	377.4	12.0	963	6 AR278586	AR278586 Sequence
41	377.4	12.0	963	6 AX141036	AX141036 Sequence
42	377.4	12.0	963	6 AX200896	AX200896 Sequence
43	377.4	12.0	963	6 AX267552	AX267552 Sequence
44	377.4	12.0	963	6 AX549376	AX549376 Sequence
45	377.4	12.0	1015	6 AX556222	AX556222 Sequence

ALIGNMENTS

RESULT 1
AX107037
LOCUS AX107037 3136 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0125434.
ACCESSION AX107037
VERSION AX107037.1 GI:13922563
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 Raitano, A.B., Afar, D.E., Jakobovits, A., Farris, M., Hubert, R.S.,
Mitchell, S.C. and Saffran, D.C.
G protein-coupled receptor up-regulated in prostate cancer and uses

Pred. No. is the number of results predicted by chance to have a

thereof
Patent: WO 0125434-A 1 12-APR-2001;
Urogenesys, Inc. (US)

Location/Qualifiers

FEATURES

Source

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133. 1086
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CDS

BASE COUNT 864 a 674 c 622 g 976 t

Query Match 100.0%; Score 3136; DB 6; Length 3136;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CAGAGAGGCTGATTTGAGTGGAGCTGCGACAGCCTCTTCTGGAGGAAGCTGGACAAAG 60
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61 GGGGTCAACATCTCTTCCATACGGTTGAGCCTTACCTGCTGGTCTGGTCAACATTC 120
121 AGCTTCTTCATGATGAGTGGATGCCAATGGCAATGAATCCAGTGTACTATCTCATCTTA 180
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Db	1801	TGGGCTCATACAGATATAAAAATTTAAAAAAAAGAGCTTCAGGCCAAATCTCATATGA	1860
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Db	1861	TGTGGAGAACTGTATGAGAGACCAACAAGGAGTGTGGAGTTTCCAGAGCTTAC	1920
QY	1921	ATTTTCTATGAGAGGTATTTAATTTCTTCTCACTATCATAGTGTGTATTTAGAAATTC	1980
Db	1921	ATTTTCTATGAGAGGTATTTAATTTCTTCTCACTATCATAGTGTGTATTTAGGAATTC	1980
QY	1981	CTGGCAACAGAACTCATGGCTTTATCCCATAGCTATTTGCTCTGCTGCATTT	2040
Db	1981	CTGGCAACAGAACTCATGGCTTTATCCCATAGCTATTTGCTCTGCTGCATTT	2040
QY	2041	GCCAAATTCCTGTGCTTGGAAAGAAATGATTTCTAGTTCAACAAATATGAAAGATCTTA	2100
Db	2041	GCCAAATTCCTGTGCTTGGAAAGAAATGATTTCTAGTTCAACAAATATGAAAGATCTTA	2100
QY	2101	TTCAAGAAAGTCTGCATAGGGCTTATAGCAAGTTATTTTATTAAGTTCCATAGGTGA	2160
Db	2101	TTCAAGAAAGTCTGCATATAGGCTTATAGCAAGTTATTTTATTAAGTTCCATAGGTGA	2160
QY	2161	TTCTGATATGAGCAGTGAAGTTAGGAGCCACAGATATATGAGGAAGTATGAAATGGCAGG	2220
Db	2161	TTCTGATATGAGCAGTGAAGTTAGGAGCCACAGATATATGAGGAAGTATGAAATGGCAGG	2220
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Db	2281	AGGACCAATGCTTTATTTGGGGCTTTGTGCATATGAGAAACAAGGACTTTGAGAACCAAGGAA	2340
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Db	2341	GCAATCTGACTTATGAGCATAGGGAATCAGGCATTTTGTCTCGAAGGGGTATATACAAAGGG	2400
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QY	2461	AAATATCTTAAACATGTGATCATATATGTGTAGTTTCATTTCTTTCATATCTCAGG	2520
Db	2461	AAATATCTTAAACATGTGATCATATATGTGTAGTTTCATTTCTTTCATATCTCAGG	2520
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Db	2521	TTCCCTGATATGGAATTCCTATTAACATGTTTCAATCCCTTTTGTATGAGATATATATTT	2580
QY	2581	GGAATGCTTATTAATATCTTGTATTTGGTCTGGAAGTGAAGCCATGAGGCACTGTT	2640
Db	2581	GGAATGCTTATTAATATCTTGTATTTGGTCTGGAAGTGAAGCCATGAGGCACTGTT	2640
QY	2641	TATATATGAATGTATCTGTGTATCATATGACATGCTTTTGCTCATCATTTGATATCCCC	2700
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Db	2821	TTATTAATTTCTGGCCATTAATCTTCAATGTGAGTGAAGTGAACATGTGCATTTCTATAC	2880
QY	2881	CTGGCTATTAACCTTCCCATGTGACGCTTTTCAATGTGACATTAATATGTAATCTTGGGA	2940

[illegible]

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Oy		2581	GGAATATGCCATTTAATATCTTGATTTTGCTGCTGGACTGTAAAGCCATTAAGGGCAGTGT	2640
Db		2581	GGAATATCCATTTAATTAATCAATGATTTATGTGCTGCTGAGCTGTAAAGCCATTAAGGGCAGTGT	2640
Oy		2541	TATATATGAATAGTATCTCTGTTATATATATGATATGATACGCCTTTGGCTATCAATTTGCCCC	2700
Db		2541	TATATATGAATAGTATCTCTGTTATATATATGATATGATACGCCTTTGGCTATCAATTTGCCCC	2700
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Db		2701	AGCAAAGTGCTTAGAACATAAATAGTCTTATAGCTTGAACCGGTTATTTTTTCATCAACC	2760
Oy		2761	TGATTCCTCTGCTGCTTGAACAATAGCCAGATTTTCCAGCCTTCTTGAGTTGGGTA	2820
Db		2761	TGATTCCTCTGCTGCTTGAACAATAGCCAGATTTTCCAGCCTTCTTGAGTTGGGTA	2820
Oy		2821	TTATTAATTCCTGGCCATTAACCTTCCAATGTGAGTGAAGAATGACATGTGCATTTCTATAC	2880
Db		2821	TTATTAATTCCTGGCCATTAACCTTCCAATGTGAGTGAAGAATGACATGTGCATTTCTATAC	2880
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Db		3001	GCCAAACCTCTGTCAATTGCAAGTCCCACTTGATTTGTACAGAGCAGTTGGATPAAGTA	3060
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Db		3121	AAAAAAAAAAAAAAAAAAAA 3136	
RESULT_3				
HSM804438				
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DEFINITION			Homo sapiens mRNA; cDNA DKFZp13F0432 (from clone DKFZp13F0432).	
ACCESSION			AL8313127	
VERSION			AL8313127.1 GI:21733749	
KEYWORDS				
SOURCE				
ORGANISM			Homo sapiens (human)	
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3077) Bloecher,H., Boecher,M., Mewes,H.W., Well,B., Amid,C., Osanger,A., Fodor,G., Han,M. and Wiemann,S.	
REFERENCE			Direct Submission Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkz-heidelberg.de; Sequenced by GBF (National Research Centre for Biotechnology Ltd., Brunswickweig/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp13F0432) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clonesrzd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/. Location/Qualifiers 1..3077	
TITLE				
JOURNAL				
COMMENT				
FEATURES				
Source				

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DH10B; sites Sfi1A + Sfi1B"
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ORIGIN

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Query Match	96.5%;	Score 3025.8;	DB 9;	Length 3077;
Best Local Similarity	99.4%;	Pred. No. 0;		
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Db	62	CTGGTGCTGGTCA	CAAGTTCAAGCTTCTTCATGATGAGTGGATCCAAATGGCAATGATCAAG	121	
QY	162	TGCTAATATCTTCAT	ATCCATATGAGGCTCCCGGTTTAGAAGAGGCTCAAGTTCCGGTTGGC	221	
Db	122	TGCTAATATCTTCAT	ATCCATATGAGGCTCCCGGTTTAGAAGAGGCTCAAGTTCCGGTTGGC	181	
QY	222	CTTCCCATTTGCTCTCCCTCTACCTTACCTTATTTGCTGTCAGGTAACTGTGACAATCATCTACAT	281		
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QY	282	TGTGGGAACTGAGCA	CAAGCTTGCAATGAGCCCAATGATATATTTCTTTGATGCTTTCAAG	341	
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QY	342	CATGACATCTCATATCTCCACTATCCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAA	401		
Db	302	CATGACATCTCATATCTCCACTATCCATCCATGCCCAAAATGCTGGCCATCTTCTGGTTCAA	361		
QY	402	TTTCACATACCATCA	AGTTGATGCTTGTCTGTACAGATTTTTCGATCCATCCACTGCTTATC	461	
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QY	462	TGGCATTGAAATCA	CAGATGCTGCTGGCCATGAGCTTTTGAACCGCTATGTGGCAATCTGTCA	521	
Db	422	TGGCATTGAAATCA	CAGATGCTGCTGGCCATGAGCTTTTGAACCGCTATGTGGCAATCTGTCA	481	
QY	522	CCCACTGGCCGAC	CATGCCACAGTACTTAAGTTGGCTGTGCACCAAAATTTGGTGTGGCTGC	581	
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Db	542	TGTGTGCGGGGGGCTGCA	CTGATGAGCAACCCCTTCTGTGCTTCAATCAAGACGCTGCCCTT	601	
QY	642	CTGGCGCTGCATAT	TCTTTCCCATTTCTCTACATGCTGCTACACCAAAATGTCAATGAAGCTGGC	701	
Db	602	CTGGCGCTGCATAT	TCTTTCCCATTTCTCTACATGCTGCTACACCAAAATGTCAATGAAGCTGGC	661	
QY	702	CTGTGATGATATCGGGGTCA	TGTGTGTATGTGGCTTATCTGTCAATCATCTTCGCAATTTGG	761	
Db	662	CTGTGATGATATCGGGGTCA	TGTGTGTATGTGGCTTATCTGTCAATCATCTTCGCAATTTGG	721	
QY	762	CTGTGACTCACTTCTCAT	TCTCTTCTCATATCTGCTTATCTTAAAGACTGTGTGGGCTT	821	
Db	722	CTGTGACTCACTTCTCAT	TCTCTTCTCATATCTGCTTATCTTAAAGACTGTGTGGGCTT	781	
QY	822	GAAACGTGAAGCCCA	AGGCCCAAGGCAATTTGGCACTTGGGCTCTCATGTGTGTGGCTGTT	881	
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[illegible]

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Db	1979	TTATGTGCTGGTCCAAATGCGCAATTACCTGTGCTTTGGAAAGATGATTTCTAGTTCA	2038
Qy	2082	CCATTATGGAAAGATTCTTATTCAGAAAGTCGTCATAGGGCTTATAGCAAGTATTTATT	2144
Db	2039	CCATTATGGAAAGATTCATTATTCAGAAAGTCGTCATAGGGCTTATAGCAAGTATTTATT	2098
Qy	2142	TTAAAGTCCATAGTGAATTCGTAGAGCAGTGGTTAGGAGCCCACTTATGATG	2201
Db	2099	TTAAAGTCCATAGTGTGTTCTGTATAGGAGTGAAGTTAGGAGCCCACTTATGATG	2158
Qy	2202	GGAAGTATGGAATGGCAGTCTTGAAGATACATTGGGCTTTTGAGTGTACTGTAAGCT	2266
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Qy	2262	GAAAAGTAGGAAATCTTCAGAGCCATGCTTTATTTGGGAGCTTTTGAGCATGGAAGAG	2322
Db	2219	GGAAGTAGGAGGAATCTTCAGAGCCATGCTTTATTTGGGAGCTTTTGAGCATGGAAGAG	2276
Qy	2332	GCACTTTGAACACGAGAAAGCAATCTGACTTAGGCAATGGATGACGCAATTTTGCTCT	2381
Db	2279	GCACTTTGAACCGGAGAAAGCAATCTGACTTAGGCAATGGATGACGCAATTTTGCTCT	2338
Qy	2382	GAGGGGCAATTACCAAGGGCTTAATAGGTTTCATCTTCAAACGAGATATGACAAACGTGTA	2444
Db	2339	GAGGGGCAATTACCAAGGGCTTAATAGGTTTCATCTTCAAACGAGATATGACAAACGTGTA	2398
Qy	2442	ACCAAGAAACTCAAATTACAAATACATACTAAACATGTGATCATATATGTGTAGTTTCAT	2501
Db	2399	ACCAAGAAACTCAAATTACAAATACTAAACATGTGATCATATATGTGTAGTTTCAT	2458
Qy	2502	TTCTTTTTCATCTCGAGTCTCCGTGATATAGATTTCTATTAACATGCTTTATCCCTTT	2566
Db	2459	TTCTTTTTCATCTCGAGTCTCCGTGATATAGATTTCTATTAACATGCTTTATCCCTTT	2518
Qy	2562	TGTATGATATCATATTTGGAAATGCGTAATTTATACCTTGTATTTGGCTGTCGACTGTA	2621
Db	2519	TGTATGATATCATATTTGGAAATGCGTAATTTATACCTTGTATTTGGCTGTCGACTGTA	2578
Qy	2622	AGCCCATGAGGGCACTGTTATTTATGATGTCACTCTGTTCACTATGACCTGCTTT	2681
Db	2579	AGCCCATGAGGGCACTGTTATTTATGATGTCACTCTGTTCACTATGACCTGCTTT	2638
Qy	2682	GCTCATCATTTGAATCCCGCAGCAAAAGTCCAGCAACATATAGGCTTATCTTGACACC	2741
Db	2639	GCTCATCATTTGAATCCCGCAGCAAAAGTCCAGCAACATATAGGCTTATCTTGACACC	2698
Qy	2742	GGTATTTTTTCATCAAACTGTATCTTCTGTCTGTAACAATAGCCAGCAATTTTCCA	2801
Db	2699	GGTATTTTTTCATCAAACTGTATCTTCTGTCTGTAACAATAGCCAGCAATTTTCCA	2758
Qy	2802	GCCCTCTTTGAGTGGGATTTATTTAAATTCGCGCATTACTTCCAAATGTAGTGGAAAGTG	2861
Db	2759	GCCCTCTTTGAGTGGGATTTATTTAAATTCGCGCATTACTTCCAAATGTAGTGGAAAGTG	2818
Qy	2862	ACATGTGCAATTTCTATACCTGCTCATTAACCCCTCCCATGTGACAGCTTTCACTGTGA	2921
Db	2819	ACATGTGCAATTTCTATACCTGCTCATTAACCCCTCCCATGTGACAGCTTTCACTGTGA	2878
Qy	2932	CATTAAATGTGACTTTGGGAAGCTATGTGTTAACAAGATTAATACAGAAAGCTGGAT	2981
Db	2879	CATTAAATGTGACTTTGGGAAGCTATGTGTTAACAAGATTAATACAGAAAGCTGGAT	2938
Qy	2982	TCTGAAAAAACTGTGACAGAGCAAACTCTGTCACTTGTGCAACTCCCACTGTATTTGTAC	3041
Db	2939	TCTGAAAAAACTGTGACAGAGCAAACTCTGTCACTTGTGCAACTCCCACTGTATTTGTAC	2998
Qy	3042	GAGGCACTTGGATAGTGAATAATTAAGTACTATGTGTCAAGAAAAAATTTTTTTTTTTT	3101

Db	2999	GAGGAGTGTGATAGTAAAAATAAATACATCTGTGTCAAGTCTCCAAAAA	3056
Cy	3102	AAAAAAAAAAAAAAAAAAAA	3120
Db	3059	AAAAAAAAAAAAAAAAAAAA	3077
RESULT 4	AC105936/c		
LOCUS	AC105936	175073 bp	DNA linear HTG 11-JAN-2002
DEFINITION	Homo sapiens chromosome 3 clone RP11-27N2, WORKING DRAFT SEQUENCE,		
ACCESSION	9 unoriented pieces.		
VERSION	AC105936 AC027367		
KEYWORDS	AC105936.1 GI:18129413		
SOURCE	HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTROP; HTGS_ACTIVEFIN.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 175073)		
JOURNAL	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
AUTHORS	Direct Submission		
TITLE	Unpublished		
REFERENCE	2 (bases 1 to 175073)		
JOURNAL	Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.		
AUTHORS	Direct Submission		
TITLE	Submitted (11-JAN-2002) Genome Center, University of Washington,		
KEYWORDS	Box 357145, Seattle, WA 98195, USA		
COMMENT	On Jan 11, 2002 this sequence version replaced gi:18072576.		
	----- Genome Center -----		
	Center: University of Washington Genome Center		
	Center Code: UWG		
	Web site: http://www.genome.washington.edu		
	Contact: uwgchgs@u.washington.edu		
	Drafting Center: BCM		
	----- Project Information -----		
	Center project name: chr-3		
	Center clone name: RP11-27N2 (bc0744)		
	----- Summary Statistics -----		
	Sequencing vector: plasmid; 100% of reads		
	Chemistry: Dye-terminator ET; 67% of reads		
	Chemistry: Dye-terminator Big Dye; 33% of reads		
	Assembly program: Phrap; version 0.99019		
	Consensus quality: 169829 bases at least Q40		
	Consensus quality: 172659 bases at least Q30		
	Consensus quality: 173890 bases at least Q20		
	Insert size: 185500; 10.7% error; agarose-fp		
	Insert size: 174273; sum-of-contigs		
	Quality coverage: 6.4x in Q20 bases; agarose-fp		
	Quality coverage: 6.8x in Q20 bases; sum-of-contigs		

	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 9 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		

	* 1 3647: contig of 3647 bp in length		
	* 3648 3747: gap of unknown length		
	* 3748 14302: contig of 10555 bp in length		
	* 14303 14402: gap of unknown length		
	* 14403 19751: contig of 5349 bp in length		
	* 19752 19852: gap of unknown length		
	* 19852 31134: contig of 11283 bp in length		
	* 31135 31234: gap of unknown length		
	* 31235 51216: contig of 19982 bp in length		
	* 51217 51316: gap of unknown length		
	* 51317 81029: contig of 29713 bp in length		
	* 81030 81129: gap of unknown length		
	* 81130 102621: contig of 21492 bp in length		
	* 102622 102721: gap of unknown length		

[illegible]

Db	174253	CTGCTTCATCAAGCAAGCTGCCCTTCTGCGCTCCAAATCCCTTCCATCTCACTGACC	174195
OY	677	TACACCAAGATGTCATGAAGCTGAGCTGAGATGATATCCGGGTGCATATGCGTATAGGCC	736
Db	174193	TACACCAAGATGTCATGAAGCTGAGCTGAGATGATATCCGGGTGCATATGCGTATAGGCC	174133
OY	737	TTATGTCATCATCTCCGCCATTGGCGCTGAGCTCACTCTCATCTCTTCTCATATCTGC	796
Db	174133	TTATGTCATCATCTCCGCCATTGGCGCTGAGCTCACTCTCATCTCTTCTCATATCTGC	174074
OY	797	TTATCTTAAAGACTGTGTGAGCTGTGACAGAGAACCCAGGCCCAAGGACTTTGGCACTT	856
Db	174073	TTATCTTAAAGACTGTGTGAGCTGTGAGAGAACCCAGGCCCAAGGACTTTGGCACTT	174014
OY	857	GCGTCTCATGTGTGTGTGTGTTCATATTCATATGTACCTTTCATTTGATGTCATGG	916
Db	174013	GCGTCTCATGTGTGTGTGTGTTCATATTCATATGTACCTTTCATTTGATGTCATGG	173954
OY	917	TGCATGCGCTTTAGACAGCGGCGGATCTCCGCTGCGCTCATCTTGGCCAAATCTATC	976
Db	173993	TGCATGCGCTTTAGACAGCGGCGGATCTCCGCTGCGCTCATCTTGGCCAAATCTATC	173894
OY	977	TGCTGTCTCTCTGTGTGTCTCAACCAATGTGTATGAGTGAAGACAAGAGATTTGAC	1036
Db	173893	TGCTGTCTCTCTGTGTGTCTCAACCAATGTGTATGAGTGAAGACAAGAGATTTGAC	173834
OY	1037	AGCGCATCTTCGACCTTTTCCATGTGTGCGACACACGCTTCAGAGCCTTAGGTCACTGA	1096
Db	173833	AGCGCATCTTCGACCTTTTCCATGTGTGCGACACACGCTTCAGAGCCTTAGGTCACTGA	173774
OY	1097	TCAAACCTCTCTTCCATTCGAGATCTCTGATTCAGATTTTAAATGTAACCTTTGGAG	1156
Db	173773	TCAAACCTCTCTTCCATTCGAGATCTCTGATTCAGATTTTAAATGTAACCTTTGGAG	173714
OY	1157	ACAGATTCGAAAAAAATTTCTTAAATPAAAAATACAACCTCAATCTTCAAAATGTA	1216
Db	173713	ACAGATTCGAAAAAAATTTCTTAAATPAAAAATACAACCTCAATCTTCAAAATGTA	173655
OY	1217	AACGTGTGGGGAATCCATTTTTCATATATATTTCTTCTTGTTCCTTGCTACAT	1276
Db	173654	AACGTGTGGGGAATCCATTTTTCATATATATTTCTTCTTGTTCCTTGCTACAT	173595
OY	1277	ATAATTAATTAATACCTGACATGAGTGTGTGTGAGGGTATTAATCTTTTCAATTACAT	1336
Db	173594	ATAATTAATTAATACCTGACATGAGTGTGTGTGAGGGTATTAATCTTTTCAATTACAT	173535
OY	1337	GCAGTCCAAATCTTAACTGCTTCTACTAGTGTGTACAGCATTTCTGATTAAGATGTGA	1396
Db	173334	GCAGTCCAAATCTTAACTGCTTCTACTAGTGTGTACAGCATTTCTGATTAAGATGTGA	173475
OY	1397	CATCTAGAGAACATTTGGCAAAAGGCGCTAAGCAGCGCAAGAGAAATPAAACAGAAATATA	1456
Db	173474	CATCTAGAGAACATTTGGCAAAAGGCGCTAAGCAGCGCAAGAGAAATPAAACAGAAATATA	173415
OY	1457	ATAAAATGAGATATCTAGCTTAAAACTATAATCTTCTCTTCAAGACTCCCAACCAATT	1516
Db	173414	ATAAAATGAGATATCTAGCTTAAAACTATAATCTTCTCTTCAAGACTCCCAACCAATT	173355
OY	1517	GGATCTCAGAAAAATGCTGTCTTCAAAATGACTTGTACAGAGAAATPAAATTTTCTCTC	1576
Db	173354	GGATCTCAGAAAAATGCTGTCTTCAAAATGACTTGTACAGAGAAATPAAATTTTCTCTC	173295
OY	1577	TGAGCATGACACTTAAGGGGAGAGATGGAAGTAAGCTTGAAAGAGTACTTTAAGCT	1636
Db	173294	TGAGCATGACACTTAAGGGGAGAGATGGAAGTAAGCTTGAAAGAGTACTTTAAGCT	173235
OY	1637	ACGTTATGAAATGTATACACATGTTCTGAGAGTTTTCACAGCATATGAGACCGGTTTTT	1696
Db	173234	ACGTTATGAAATGTATACACATGTTCTGAGAGTTTTCACAGCATATGAGACCGGTTTTT	173175
OY	1697	CGTATTTAATTTCTTATCAACCTTTTAATTAGGCAAGATATTATTAGTACCTCATTTG	1756

Db	173174	CCATATTAAATTTTCTTATCAACCCCTTAATTATGAGCAAAAGATATTATTAGACCCCTATTG	173115
Qy	1757	TAGCCATGGGAAATTTGATNGTTCAAGTGGGGATCAGTGAATTAAATGGGCTCATACAAATA	1816
Db	173114	TAGCCATGGGAAATTTGATNGTTCAAGTGGGGATCAGTGAATTAAATGGGCTCATACAAATA	173055
Qy	1817	TAAAAATTAAAAAAGAACTTCATGCCCATCTCATATGATGTGGAGAACTGTTA	1876
Db	173054	TAAAAATTTAAAAAAGAACTTCATGCCCATCTCATATGATGTGGAGAACTGTTA	172997
Qy	1877	GAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGCTTTCATTTTCTAGAGAGGT	1936
Db	172996	GAGAGACCAACAGGGTAGTGGGTTAGAGATTTCCAGAGCTTTCATTTTCTAGAGAGGT	172937
Qy	1937	ATTATATTTCTTCTCACTCATCAGTGTGTATTAAGAAATTTCCGGCAACGAAGCTCA	1996
Db	172936	ATTATATTTCTTCTCACTCATCAGTGTGTATTAAGAAATTTCCGGCAACGAAGCTCA	172877
Qy	1997	TGGCTTTAATCCCACTAGCTATTTGCTTATTTGCTGGTCCAAATGGCAATACCTGTGTC	2056
Db	172876	TGGCTTTAATCCCACTAGCTATTTGCTTATTTGCTGGTCCAAATGGCAATACCTGTGTC	172817
Qy	2057	TTGGAAGAGATATTTCTAGGTTCACCAATATGAAAGATCTTATTCAGAAGTCCGAAAT	2116
Db	172816	TTGGAAGAGATATTTCTAGGTTCACCAATATGAAAGATCTTATTCAGAAGTCCGAAAT	172755
Qy	2117	AGGGCTTATAGCAAGTTATTAATTTTAAAGTTCATAGTGATTTCTGATAGGAGTGA	2176
Db	172756	AGGGCTTATAGCAAGTTATTAATTTTAAAGTTCATAGTGATTTCTGATAGGAGTGA	172697
Qy	2177	GGTTAGGGAGCCACAGTTATGATGGGAAGTATGAAATGGCAGGCTTGAAGATTAATT	2236
Db	172696	GGTTAGGGAGCCACAGTTATGATGGGAAGTATGAAATGGCAGGCTTGAAGATTAATT	172637
Qy	2237	GGCCTTTTGAAGTGAAGCTGTAGCTGGAAGAGGAGATCTTCAGAGCAATGCTTATT	2296
Db	172636	GGCCTTTTGAAGTGAAGCTGTAGCTGTAGGAAAGGAGGAATCTTCAGAGCAATGCTTATT	172577
Qy	2297	TGGGGCTTTGTGCAATATGAAACAGGACTTTGAAACAGGAAGCAATCTGACTTAAGGC	2356
Db	172576	TGGGGCTTTGTGCAATATGAAACAGGACTTTGAAACAGGAAGCAATCTGACTTAAGGC	172517
Qy	2357	ATGGAAATCAGGACTTTTGTGCTTGAAGGGCTATTAACAAGGTTAATAGGTTTCACTC	2416
Db	172516	ATGGAAATCAGGACTTTTGTGCTTGAAGGGCTATTAACAAGGTTAATAGGTTTCACTC	172457
Qy	2417	TCAACAGGATATGACAAAGTGTATACCAAGAACTCAAAATTAATAATCTAAAAATGT	2476
Db	172456	TCAACAGGATATGACAAAGTGTATACCAAGAACTCAAAATTAATAATCTAAAAATGT	172397
Qy	2477	GATCATATATGTGGTAAGTTTCAATTTTCTTTTCAATCCTCAGGTTCCTGTATAGGAT	2536
Db	172396	GATCATATATGTGGTAAGTTTCAATTTTCTTTTCAATCCTCAGGTTCCTGTATAGGAT	172337
Qy	2537	CCATATAATGCTTTCATCCCTTTTGTATATGATATCAATAATGGAAATGCCATTTTA	2596
Db	172336	CCATATAATGCTTTCATCCCTTTTGTATATGATATCAATAATGGAAATGCCATTTTA	172277
Qy	2597	TACTGTATTTGGCTGAGACGTATGAAGCCCAAGAGGAGCACTTTATATATGAATGTCA	2656
Db	172276	TACTGTATTTGGCTGAGACGTATGAAGCCCAAGAGGAGCACTTTATATATGAATGTCA	172217
Qy	2657	CTGTGTTCATCATTTGACTCTCTTTTGTCAATCATTTGAATTCGCCCAAGAGTCCTAGAA	2716
Db	172216	CTGTGTTCATCATTTGACTCTCTTTTGTCAATCATTTGAATTCGCCCAAGAGTCCTAGAA	172157
Qy	2717	CATAATAGTGTATATGCTTGAACACCGGTTATTTTGAACAAACCTGATTCCTGTGCTCT	2776
Db	172156	CATAATAGTGTATATGCTTGAACACCGGTTATTTTGAACAAACCTGATTCCTGTGCTCT	172097
Qy	2777	GAACAACATAGCACAGCAATTTTCCAGCTTCTTTGAGTGTGGATATTAATTTTGCC	2836
Db	172096	GAACAACATAGCACAGCAATTTTCCAGCTTCTTTGAGTGTGGATATTAATTTTGCC	172037

[illegible]

QY 1037 AGGCGATCCTTGGACCTTTCCATGTGGCCACACAGCTTACAGCCCTAGAGCTGACGTGA 1096
DB 55402 AGGCGATCCTTGGACCTTTCCATGTGGCCACACAGCTTACAGCCCTAGAGCTGACGTGA 55343
QY 1097 TCAACTCTCTTTCCATTCAGAGCTCCGATTCACATTTTAACTTTAATTTTGAAG 1156
DB 55342 TCAACTCTCTTTCCATTCAGAGCTCCGATTCACATTTTAACTTTAATTTTGAAG 55283
QY 1157 ACAATATTCAGAAAAAAATTTCCCTAATAAAAAATACACATCAGATCCCTCAATATGA 1216
DB 55282 ACAATATTCAGAAAAAAATTTCCCTAAT - AAAAAATACACATCAGATCCCTCAATATGA 55224
QY 1217 AACTGTGGGGGAAATCTCCATTTTTCATATTTTCTCTTGTGTTTCTTGTGCTACT 1276
DB 55223 AACTGTGGGGGAAATCTCCATTTTTCATATTTTCTCTTGTGTTTCTTGTGCTACT 55164
QY 1277 ATAATTTAATATCCTGATAGTGTGGTTAGAGGTTAATTAATTTTCAATTTTACAT 1336
DB 55163 ATAATTTAATATCCTGATAGTGTGGTTAGAGGTTAATTAATTTTCAATTTTACAT 55104
QY 1337 GCACTCCAAATCTTAACCTGCTTACTGATGTGTTACAGATTTCTGATTAAGATGTGA 1396
DB 55103 GCACTCCAAATCTTAACCTGCTTACTGATGTGTTACAGATTTCTGATTAAGATGTGA 55044
QY 1397 CATCTAGAGAACTTTGCCAAGGCTTAAGCAGGCAAGGAAATTAACAGATATTA 1456
DB 55043 CATCTAGAGAACTTTGCCAAGGCTTAAGCAGGCAAGGAAATTAACAGATATTA 54984
QY 1457 ATAAATAGATATCTAGCTTAAACTATTAATTTCTCTTCCAGAACTCCCAACCAT 1516
DB 54983 ATAAATAGATATCTAGCTTAAACTATTAATTTCTCTTCCAGAACTCCCAACCAT 54924
QY 1517 GGATCTCAGAAAAATGCTGTCTTCAAATGATCTTACAGAGAAATTAATTTTCTCTC 1576
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QY 1577 TGGACATAGACATTTAAGGGAAGATGGAATGAAAGCTTGAAGAGATCAATTAAGT 1636
DB 54863 TGGACATAGACATTTAAGGGAAGATGGAATGAAAGCTTGAAGAGATCAATTAAGT 54804
QY 1637 ACGTTATGAAGTTGACACATGTTCTGAGAGTTTCAACAGATATGAACCTGTGTTT 1696
DB 54803 ACGTTATGAAGTTGACACATGTTCTGAGAGTTTCAACAGATATGAACCTGTGTTT 54744
QY 1697 CCTATTATTTTCTTATCAACCTTATTAATTAAGCAAGATATTAATTAAGCAACCTGAT 1756
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DB 54683 TAGCCATGGGAAATGATGTTCAGTGGGATCAGTGAATTAATGGGTCATACAGTA 54624
QY 1817 TAAAAATTAATAAAAAAAGAACTTCATGGCCAACTCATAATGATGGAAGAACTGTA 1876
DB 54623 TAAAAATTAATAAAAAAAGAACTTCATGGCCAACTCATAATGATGGAAGAACTGTA 54566
QY 1877 GAGAGACCAACAGGAGTGTGGGTTAGAGATTTCCAGAGCTTACATTTTCTAGAGAGGT 1936
DB 54565 GAGAGACCAACAGGAGTGTGGGTTAGAGATTTCCAGAGCTTACATTTTCTAGAGAGGT 54506
QY 1937 ATTATATTTCTTCTCATCTCATCCAGTGTGTATTTAGAGATTTCTGGCAACGAATCTCA 1996
DB 54505 ATTATATTTCTTCTCATCTCATCCAGTGTGTATTTAGAGATTTCTGGCAACGAATCTCA 54446
QY 1997 TGGCTTATATCCCACTAGCTATGCTTATGCTGTGCTCAATTTGCAATTAACCTGTGTC 2056
DB 54445 TGGCTTATATCCCACTAGCTATGCTTATGCTGTGCTCAATTTGCAATTAACCTGTGTC 54386
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DB 54265 GGTTAGGGAGGCCACAGTATATAGGGAAGTATGGAATGCGAGGCTTGAAGATTAACAT 54206
QY 2237 GGCCTTTTGAAGTGTGACTGTAGCTGGAAGATGGAAGATTTCTGAGAACATGCTTAT 2296
DB 54205 GGCCTTTTGAAGTGTGACTGTAGCTGGAAGATGGAAGATTTCTGAGAACATGCTTAT 54146
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DB 54145 TGGGCTTTTGTGCAATATGGAACAGGACCTTGAACAGGAAGCAATCTGATAGGC 54086
QY 2357 ATGGAAATCAGGCAATTTTGTGCTTGTGAGGGGCTATTAACAAGGTTAATAGTTTCA 2416
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QY 2477 GATCATATATGTGTAAGTTCATTTTCTTTTCAATCCCTGAGTCCCTGATATGAT 2536
DB 53965 GATCATATATGTGTAAGTTCATTTTCTTTTCAATCCCTGAGTCCCTGATATGAT 53906
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DB 53725 CATATATGCTTATGCTTATGACACCGGTATTTTTCATCAAACTGATTTCTTCTGCT 53666
QY 2777 GAACACATAGCCAGCAATTTTCCAGCTTCTTGAAGTGGGATTTAATTTCTGACC 2836
DB 53665 GAACACATAGCCAGCAATTTTCCAGCTTCTTGAAGTGGGATTTAATTTCTGACC 53606
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DB 53605 ATTACTTCAATGTAGTGAAGTGAAGTGAATTTCTATACCTGCTCATAAACC 53546
QY 2897 TCCCATGTGACCTTTTCAATGTGACATTAATGATCTTGAAGAGTATGTTACACA 2956
DB 53545 TCCCATGTGACCTTTTCAATGTGACATTAATGATCTTGAAGAGTATGTTACACA 53486
QY 2957 GAGTAAATCAACAGAGGCTGATTTCTGAAAAAAAGTGTGAGAGCCAACTGTGAT 3016
DB 53485 GAGTAAATCAACAGAGGCTGATTTCTGAAAAAAAGTGTGAGAGCCAACTGTGAT 53426
QY 3017 TTGCAATCTCCCACTGTATTTTGTACAGAGGCTTGAATAGTGAATAAAGTACTAT 3076
DB 53425 TTGCAATCTCCCACTGTATTTTGTACAGAGGCTTGAATAGTGAATAAAGTACTAT 53366
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DB 53365 GTGTCAAGTCTGTAAAA 53348

RESULT 6
AA201144
LOCUS AA201144 2061 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 774 from Patent WO0151633.

ACCESSION AX201144
VERSION AX201144.1 GI:15390908
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,
Stolk, J.A., Skelly, Y.A., Wang, A. and Mesgher, M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 774 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
1..2061
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 612 a 383 c 399 g 667 t
ORIGIN
Query Match 64.7%; Score 2028.4; DB 6; Length 2061;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 1029 GATTGAGACGGGATCCCTTCGATCTTCGATGAGGCCACACGCTTCAGAGCCCTAGGT 1088
DB 3 GATTGAGACGGGATCCCTTCGATCTTCGATGAGGCCACACGCTTCAGAGCCCTAGGT 62
QY 1089 GTGAGTGATCAAACTCTCTTCATTCAGAGTCCCTGATTCAGATTATATGTTAAT 1148
DB 63 GTGAGTGATCAAACTCTCTTCATTCAGAGTCCCTGATTCAGATTATATGTTAAT 122
QY 1149 TTTGGAACACGATATTCGAAAAAAATTTCTTATATATATATATATATATATATATAT 1208
DB 123 TTTGGAACACGATATTCGAAAAAAATTTCTTATATATATATATATATATATATATAT 181
QY 1209 AAATATGAACGTGGTGGGGAATCTCCATTTTTCATATATATATATATATATATATAT 1268
DB 182 AAATATGAACGTGGTGGGGAATCTCCATTTTTCATATATATATATATATATATATATAT 241
QY 1269 TGTCTAT 1328
DB 242 TGTCTAT 301
QY 1329 TTTACCATGACATCCAAATCTTAATCTGCTTACTGATGTTTACAGCATTCGAGATA 1388
DB 302 TTTACCATGACATCCAAATCTTAATCTGCTTACTGATGTTTACAGCATTCGAGATA 361
QY 1389 GAATGTATCATCTAGAGAACTTTGCCAAGGCTTAAGCAAGGCAAGAAATTAACAC 1448
DB 362 GAATGTATCATCTAGAGAACTTTGCCAAGGCTTAAGCAAGGCAAGAAATTAACAC 421
QY 1449 AGAAT 1508
DB 422 AGAAT 481
QY 1509 ACCACATGATCTCAGAAAAATCTGCTTCAAAATGACTTCTACAGAGAAATTAAT 1568
DB 482 ACCACATGATCTCAGAAAAATCTGCTTCAAAATGACTTCTACAGAGAAATTAAT 541
QY 1569 TTTTCTCTGAGACCTAGCACTTAAGGGGAGATTTGAAGTAAAGCTTGAAGAGTAC 1628
DB 542 TTTTCTCTGAGACCTAGCACTTAAGGGGAGATTTGAAGTAAAGCTTGAAGAGTAC 601
QY 1629 ATTATACCTAT 1688
DB 602 ATTATACCTAT 661
QY 1689 CTGTTTTCTAT 1748

DB 662 CTGTTTTCTAT 721
QY 1749 CCTCATTTGATGACATGGGAAAAATGATGTTTCAGTGGGGATCATGAAATTAATGGGGTCA 1808
DB 722 CCTCATTTGATGACATGGGAAAAATGATGTTTCAGTGGGGATCATGAAATTAATGGGGTCA 781
QY 1809 TACAGTAT 1868
DB 782 TACAGTAT 839
QY 1869 AACTGTATAGAGACCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1928
DB 840 AACTGTATAGAGACCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 899
QY 1929 GAGAGAT 1988
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LOCUS AX267943
DEFINITION Sequence 917 from Patent WO01/73032.
ACCESSION AX267943
VERSION AX267943.1 GI:16516537
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kajos, M.D., Fanger, G.R., Reiter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.
and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer.
Patent: WO 01/73032-A, 917 04-OCT-2001;
JOURNAL CORIXA CORPORATION (US)
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Location/Qualifiers
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Query Match	Best Local Similarity	Score	DB	Length	2061;
Matches	Conservative	0;	Mismatches	1;	Indels
					Gaps
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3	GATTGACAGCGCATCTTCGACCTTTTCGATGCGCACACACGCTTCAGGCCCTAGT	10889			
1089	GTCAGTATCAAACTCTTCGATGCGCACACACGCTTCAGGCCCTAGT	11448			
63	GTCAGTATCAAACTCTTCGATGCGCACACACGCTTCAGGCCCTAGT	122			
1149	TTTGGAGACAGTATTCAGAAAAAAATTCCTTATTAATAAATCACTGATCTTC	12068			
123	TTTGGAGACAGTATTCAGAAAAAAATTCCTTATTAATAAATCACTGATCTTC	181			
1209	AAATATGAACTGGTGGGGAATCTCACTTTTCATATATTTCTCTTGTTCCT	12688			
182	AAATATGAACTGGTGGGGAATCTCACTTTTCATATATTTCTCTTGTTCCT	241			
1269	TGCTACATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	13288			
242	TGCTACATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	301			
1329	TTTACCATGACGCTCAATCTAACTCTCTCTCACTGATGCTTACAGATCTGAGATTA	13888			
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362	GAATGATACATCTTAGAGAACATTTGGCCAAAGGCTTAAGACGCGCAAGAAATTAAC	421			
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DEFINITION SEQUENCE, 8 unordered pieces.
ACCESSION AC025249
VERSION AC025249.5 GI:9958307
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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DEFINITION Sequence 773 from Patent WO0151633.
ACCESSION  AX201143
VERSION     AX201143.1  GI:15390907
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
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REFERENCE
  1. Xu, J., Dillon, P.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
    Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Reiter, M.W.,
    Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.
    Compositions and methods for the therapy and diagnosis of prostate
    cancer.
    Patent: WO 0151633-A 773 19-JUL-2001;
    CORIAX CORPORATION (US)
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Best Local Similarity 99.8%; Pred. No. 2,1e-274;
Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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Qy      172     TTGATCTAATAGGCTCCCTGTTAGAAAGAGGCTCAGTTCGCTGCTGCCATG 231
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Db      181     TGTCTCCCTTACTTATTTGCTGTGCTAGGTAACTTGACATCATCTAATTTGCGGACT 240
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Qy      352     CTGATCTCACTCATCATGTCACCAAAATGCTGGCCATCTTGTGTTCAATTCATAC 411
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```


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 QY 712 ATCCGGGTCAATGTCCTTATGAGCTTATGCTATATCTCCGCCATTGGCTGAGCTCA 771
 DB 661 ATCCGGGTCAATGTCCTTATGAGCTTATGCTATATCTCCGCCATTGGCTGAGCTCA 720
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 LOCUS AX267942
 DEFINITION Sequence 916 from Patent W00173032.
 ACCESSION AX267942
 VERSION AX267942.1 GI:16516536
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 AUTHORS Xu, J., Dillon, D.C., Mitcham, J.T., Harlocker, S.T., Jiang, Y.,
 Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
 Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A., Hepler, W.T.
 and Henderson, R.A.
 TITL Composition and methods for the therapy and diagnosis of prostate
 cancer. WO 0173032-A 916 04-OCT-2001;
 JOURNAL CORIXA CORPORATION (US)
 FEATURES
 SOURCE 1..1302
 /organism="Homo sapiens"

BASE COUNT 277 a 346 c 259 g 420 t
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 DB 481 CATGCCACAGTACTTACGTTGCTCGTGTGTCACCAAAATGGTGTGCTGTGTGGTGG 540
 QY 592 GGGGCTGCACTGATGAGCAACCCCTTCTGCTTATGTCAGAGAGCTGCCCTTCTGGCGCTCC 651
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 QY 1312 GGATTAATCTTTTCAATTTTACATGAGCTCCAAATCTTAAT 1354
 DB 1260 GGATTAATCTTTTCAATTTTACATGAGCTCCAAATCTTAAT 1302

RESULT 13
 BC022401 1225 bp mRNA linear PRI 04-FEB-2002
 LOCUS Homo sapiens, clone MGC:24137 IMAGE:4694856, mRNA, complete cds.
 DEFINITION BC022401
 ACCESSION BC022401.1 GI:18490239
 VERSION MGC.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1225)
 Strausberg, R.
 Direct Submission
 Submitted (01-FEB-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mdcpaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
 Series: ILNL Plate: 36 Row: n Column: 16.
 Location/Qualifiers
 1. 1225

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Query Match 37.8%; Score 1186.4; DB 9; Length 1225;
 Best Local Similarity 99.5%; Pred. No. 66-252;
 Matches 1190; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 DB 16 CAGAGAGGCTGTATTTCAATGACAGCTGCGCAAGCTCTCTGAGAGAGACTGACAAAG 75
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Db	1036	ACAAAGAGATTTGCAACAGGCACTCTTGAC	CTTTCCATGTGTCGACACACAGCTTCAAG	1095
QY	1081	CCCTAGGTGTCAGTATCAAACTTCTTTCCATTTCCAGAGT	CCTCTGATTCAGATTTTAAT	1140
Db	1096	CCCTAGGTGTCAGTATCAAACTTCTTTCCATTTCCAGAGT	CCTCTGATTCAGATTTTAAT	1155
QY	1141	GTATACATTTTGGAAAGACAGTATTCAGAAAAAAATTTCC	TTAATATATATATATCA	1196
Db	1156	GTATACATTTTGGAAAGACAGTATTCAGAAAAAAATTTCC	TTAATATATATATATCA	1211

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DEFINITION	Sequence 745 from Patent EP1270724.		linear
ACCESSION	AX646553		
VERSION	AX646553.1	GI:28798936	
KEYWORDS			
SOURCE	Homo sapiens (human)		

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H. Glutamine triphosphate-binding protein coupled receptors Patent: EP 1270724-A 745 02-JA-2003; National Institute of Advanced Industrial Science and Technology (JP) ; Center for Advanced Science and Technology Incubation, Ltd. (JP)

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CDS	201..1154

BASE COUNT 297 a 338 c 278 g 441 t
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Query Match	37.8%	Score 1186.2	DB 6	Length 1354
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Oy	137	TGATCCCAATGGCAATGATCGATGCTACATCACTTCATGATGAGGCTCCCTGATT	196	
Db	205	TGATCCCAATGGCAATGATCGATGCTACATCACTTCATGATGAGGCTCCCTGATT	264	
Oy	197	TAGAGAGGCTCAATTCTGTTGGCCTTCCATTGTGCTCCCTTACCTTAATGCTGTGC	256	

Dp	265	TAGAAAGAGCGCTCAGTTTCGTGTGGGCTTCCCATTTGTGTCCTCTAATTTGCTGTGGC	322
Qy	257	TAGGTAACTTGAACAATCATCTPACATTTGTGGGAGCTGAGACAAGGCTGATGAGCCCAATGT	316
Dp	325	TAGGTAACTTGAACAATCATCTPACATTTGTGGGAGCTGAGACAAGGCTGATGAGCCCAATGT	384
Qy	317	ATAATTTCTTTGGCATGTGCTTCAAGGCAATTGACATCTCTCATCTCCACTCATCAAGGCCA	376
Dp	385	ATAATTTCTTTGGCATGTGCTTCAAGGCAATTGACATCTCTCATCTCCACTCATCAAGGCCA	444
Qy	377	AAATGCTGGCCATCTTCTGTGTTCAATTCCACTAACATCCATCCAGTTGATGCTGTGTCTAC	436
Dp	445	AAATGCTGGCCATCTTCTGTGTTCAATTCCACTAACATCCAGTTGATGCTGTGTCTAC	504
Qy	437	AGATTTTGGCATCCACCTCTTATCTGGGCAATGGAATCCACAGTGTGCTGGGCAATGGCTT	496
Dp	505	AGATTTTGGCATCCACCTCTTATCTGGGCAATGGAATCCACAGTGTGCTGGGCAATGGCTT	564
Qy	497	TTGACCGCTATGTGGCCCATCTGTACACCCACTGTGGCCATGCCACAGTACTTAAGTGTGCTC	556
Dp	565	TTGACCGCTATGTGGCCCATCTGTACACCCACTGTGGCCATGCCACAGTACTTAAGTGTGCTC	624
Qy	557	GTTGTCACCAAAATTTGTTGTGGCTGTGTGTGTGGGGGGGGCTGCACTGATGGACCCCTTC	616
Dp	625	GTTGTCACCAAAATTTGTTGTGGCTGTGTGTGTGGGGGGGGCTGCACTGATGGACCCCTTC	684
Qy	617	CTGTCTTTCATCAAGAGAGCTGCCCTTCTGCGGCTCCAAATATCCTTTCCTATCTACTGAC	676
Dp	685	CTGTCTTTCATCAAGAGAGCTGCCCTTCTGCGGCTCCAAATATCCTTTCCTATCTACTGAC	744
Qy	677	TACACCAAGATGTCATGAAAGCTGTGTGTGTGTGTGTATTCGGGTCATATGTCTATGTGAC	736
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Qy	737	TTATTCGATATATCTCCGCGCATTTGGGCGCGGACTACTTTCATCTCCCTTCATATCTGC	796
Dp	805	TTATTCGATATATCTCCGCGCATTTGGGCGCGGACTACTTTCATCTCCCTTCATATCTGC	864
Qy	797	TTATTTCTTAAGACTGTGTGTGGGCTTGAACGCTGAAGCCGACGCAATTTGGCACTT	856
Dp	865	TTATTTCTTAAGACTGTGTGTGGGCTTGAACGCTGAAGCCGACGCAATTTGGCACTT	924
Qy	857	GCGCTCTCGAATGTGTGTGTGTGTGTATTTCTATTTCTATTTGATTTGTCATGTG	916
Dp	925	GCGCTCTCGAATGTGTGTGTGTGTGTATTTCTATTTGATTTGTCATGTG	984
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Dp	1045	TGCTGTGTTCTCTCTGTGCTCAACCCAAATTGTCTATGAGTGAAGACAAAGAGATTGCAC	1104
Qy	1037	AGGCGATTCCTTCGACTTTTGCATGTGGGCAACACGCTTGAGACCCTAGGTGCAGTGA	1098
Dp	1105	AGGCGATTCCTTCGACTTTTGCATGTGGGCAACACGCTTGAGACCCTAGGTGCAGTGA	1166
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Qy	1277	ATAATTTATTA 1287	
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RESULT 15	
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LOCUS	
DEFINITION	AB065787 Homo sapiens gene for seven transmembrane helix receptor, complete cds, 1801bp;CBR7TN_350.
ACCESSION	AB065787
VERSION	AB065787.1 GI:21928839
KEYWORDS	
SOURCE	Homo sapiens (human)

Tue Feb 10 06:04:23 2004

us-10-017-066a-1.rge

Page 23

Db 1344 ATATTATTAA 1354

Search completed: February 9, 2004, 19:19:58
Job time : 11169 secs

PT Novel gene designated PHOR-1, a G-protein-coupled receptor up-regulated
 PT in prostate cancer, useful as diagnostic marker and therapeutic target
 PT for cancers of prostate, kidney, uterus
 PS Claim 1, Fig 1A-D, 139pg; English.

CC The invention relates to a novel G-protein-coupled receptor up-regulated
 CC in prostate cancer, termed PHOR-1. The encoding cDNA is contained in
 CC plasmid designated p10P3A1 deposited with ATCC as Accession No. PTA-312.
 CC PHOR-1 polypeptides and polynucleotides are useful for diagnosing the
 CC presence of cancer, especially prostate, kidney, uterine, cervical,
 CC stomach or rectal cancer by determining and comparing the level of the
 CC protein or mRNA expression in test and normal tissue samples.
 CC Pharmaceutical compositions comprising PHOR-1 is useful for treating
 CC cancer. PHOR-1 proteins are useful for identifying ligands and other
 CC agents and cellular constituents that binds to PHOR-1 gene product and
 CC for generating antibodies which are useful in diagnostic, prognostic and
 CC imaging methodologies and for the treatment of prostate cancer. Cell
 CC lines expressing PHOR-1 are useful for identifying protein-protein
 CC interactions mediated by PHOR-1. The present sequence represents the
 CC human PHOR-1 (prostate homologue of olfactory receptor-1).

XX Sequence 317 AA;

Query Match 100.0%; Score 1617; DB 22; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2,8e-169;
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 241 TCVSHVCAVFIYVPIGLSMVHRSKRDSPLPYILANITYLVPPVNPPIYGVKTKEI 300
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 DB 301 RORILRPHVATHASEP 317

RESULT 2
 ID ABG6186 strand; Protein; 317 AA.

XX ABG6186;
 XX 15-AUG-2002 (first entry)
 XX Prostate cancer-associated protein #87.
 XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 XX Mammalia.
 XX WO200230268-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US32045.

PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281922P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-28589P.

XX

PA (BOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 XX WPI; 2002-471335/50.
 XX N-PSDB; ABK92202.

DR

XX

PT Detecting a prostate cancer-associated transcript in a cell in a
 PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue

XX Claim 27; Page 373; 436pg; English.

CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridize to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.

XX ABG61800-ABG61944 represent prostate cancer-associated proteins.

XX Sequence 317 AA;
 Query Match 99.8%; Score 1614; DB 23; Length 317;
 Best Local Similarity 99.7%; Pred. No. 5,9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPNGNESSATYFIIIGLPGLEAOFMLAPLCSLYLAVGNITIIYVTEHSLHEP 60
 DB 1 MDPNGNESSATYFIIIGLPGLEAOFMLAPLCSLYLAVGNITIIYVTEHSLHEP 60
 QY 61 MYFLCMLSGIDILISTSMRPMKLAIFWNSSTIIQFDACLQIFAIHISGNESTVLLAM 120
 DB 61 MYFLCMLSGIDILISTSMRPMKLAIFWNSSTIIQFDACLQIFAIHISGNESTVLLAM 120
 QY 121 ADRYVAICHPLRHATVTLTPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHY 180
 DB 121 ADRYVAICHPLRHATVTLTPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHY 180
 QY 181 CHODVMKACDDIRNVVYGLIIVISAIGDSLISFSYLLIKTVGLTREAOAKAFG 240
 DB 181 CHODVMKACDDIRNVVYGLIIVISAIGDSLISFSYLLIKTVGLTREAOAKAFG 240
 QY 241 TCVSHVCAVFIYVPIGLSMVHRSKRDSPLPYILANITYLVPPVNPPIYGVKTKEI 300
 DB 241 TCVSHVCAVFIYVPIGLSMVHRSKRDSPLPYILANITYLVPPVNPPIYGVKTKEI 300
 QY 301 RORILRPHVATHASEP 317
 DB 301 RORILRPHVATHASEP 317

Key	Location/Qualifiers
FT	1..26
FT	/label= signal_peptide
FT	8
FT	/note= "potential glycosylation site"
FT	34..52
FT	/label= transmembrane
FT	45
FT	/note= "potential glycosylation site"
FT	57
FT	/note= "potential phosphorylation site"
FT	62..83
FT	/label= signature_sequence
FT	/note= "G-protein coupled receptor"
FT	70
FT	/note= "potential phosphorylation site"
FT	91
FT	/note= "potential glycosylation site"
FT	113..129
FT	/label= signature_sequence
FT	/note= "G-protein coupled receptor"
FT	111
FT	/note= "potential phosphorylation site"
FT	180..194
FT	/label= signature_sequence
FT	/note= "G-protein coupled receptor"
FT	202..225
FT	/label= transmembrane
FT	240..255
FT	/label= signature_sequence
FT	/note= "G-protein coupled receptor"
FT	267
FT	/note= "potential phosphorylation site"
FT	272
FT	/note= "potential phosphorylation site"

MO200020590-A2.

13-APR-2000.

06-OCT-1999; 99MO-US23317.

06-OCT-1998; 98US-0167219.

06-OCT-1998; 98US-0172211.

PR 11-MAY-1999; 99US-0133585.

(INCYTE PHARM INC.

Tang YT, Yie H, Lal P, Bandhan O, Au-oung J, Reddy R, Corley NC, Giegler KJ, Gorgone GA, Baughn MR, Azimzay Y, WPI: 2000-328934/28.

N-PSDB; AAA09351.

Novel human G-protein coupled receptor proteins used in the diagnosis,

Converted to protein

PT	treatment and prevention of nervous system disorders,
CC	autoimmune/inflammatory disorders, and cell proliferative disorders
P7	such as cancer
XX	
PS	claim 1; Page 71-72; 84pp; English.
XX	
CC	This sequence encodes human G-protein coupled receptor protein (GCRP) 5.
CC	The GCRP polypeptides, polynucleotides, antibodies, antagonists and
CC	agonists may be administered to human patients for the diagnosis,
CC	treatment and prevention of nervous system disorders (e.g. epilepsy,
CC	stroke, neoplasms, Alzheimer's disease), autoimmune or
CC	inflammatory disorders, complications of cancer, hemodialysis and
CC	extracorporeal circulation, and cell proliferative disorders. They are
CC	also used to treat or prevent disorders associated with decreased or
CC	increased expression or activity of GCRP.
XX	
SQ	Sequence 318 AA; 569715
Query Match	99.8%; Score 1614; DB 21; Length 318;
Best Local Similarity	99.7%; Pred. No. 5,9e-169;
Matches 316; Conservative	1; Mismatches 0; Indels 0; Gaps 0

QY	1	IMPDGNGNESAA	YFFLLIGPGLEBEQFLA	PPCLSLYIAVAGL	LTIIYIVRTHSL	HEP	60
Db	2	MDDPNGNBSA	YFFLLIGPGLEBAQFLA	PPCLSLYIAVAGL	LTIIYIVRTHSL	HEP	61
QY	61	MYIFLCMLSG	IDLILISTSMPEKMLA	IFWNSSTTIOFDAC	LLOIFAHSLSG	MESTVLLAM	120
Db	62	MYIFLCMLSG	IDLILISTSMPEKMLA	IFWNSSTTIOFDAC	LLOIFAHSLSG	MESTVLLAM	121
QY	121	ADDRVYALCH	PIRHAATVLTLP	PRVTKIGVAAVVRGA	ALMAPLPVPIKOLP	PCRSNII	180
Db	122	ADDRVYALCH	PIRHAATVLTLP	PRVTKIGVAAVVRGA	ALMAPLPVPIKOLP	PCRSNII	181
QY	181	CEHODVMKLA	CDIRVNVVYGLIV	ISAIGLDSLLISFSY	LLIKTVLGLTRE	QAQAFG	240
Db	182	CEHODVMKLA	CDIRVNVVYGLIV	ISAIGLDSLLISFSY	LLIKTVLGLTRE	QAQAFG	241
QY	241	TCVSHVCAP	FIYVYFPIGLSMVHR	PSKRDSPLVILANT	YLVAPYLP	PIVGVTKET	300
Db	242	TCVSHVCAP	FIYVYFPIGLSMVHR	PSKRDSPLVILANT	YLVAPYLP	PIVGVTKET	301
QY	301	RQRIILRF	HFVATHASEP	317			
Db	302	RQRIILRF	HFVATHASEP	318			
RESULT 4							
ID	AAU69951	standard; Protein; 318 AA.					
AC	AAU69951,						
XX	30-JUN-2002	(first entry)					
DT	Human prostate cDNA encoded protein #85.						
DE	Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.						
XX	Homo sapiens.						
OS	Homo sapiens.						
XX	MO200173032-A2.						
PN	04-OCT-2001.						
PD	27-MAR-2001;	2001WO-US09919.					
XX	27-MAR-2000;	2000US-0536857.					
PR	09-MAY-2000;	2000US-0568100.					
PR	12-MAY-2000;	2000US-0570737.					
PR	13-JUN-2000;	2000US-0593793.					
PR	27-JUN-2000;	2000US-0605783.					
PR	10-AUG-2000;	2000US-0636215.					

29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Fanger GR, Ketter WM, Stolk JA, Day CH, Vedvick TS, Carter D,
 PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
 DR WPI; 2001-639232/73.
 DR N-PSDB; AAS64174, AAS64176, AAS64177.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS Claim 2; Page 568-569; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumor protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polypeptide of the invention.
 CC
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1614; DB 22; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVDPNNGSSATYFLLIGLPGLERQFPLAFPLCSLYLVVIGNLTIIYVREHSHSEP 60
 DB 2 MVDPNNGSSATYFLLIGLPGLERQFPLAFPLCSLYLVVIGNLTIIYVREHSHSEP 61
 QY 61 MYFLCMISGIDIIISSTSMKMLAIFWNSTTIQDACLLOIFAHISLGMESTYLLAM 120
 DB 62 MYFLCMISGIDIIISSTSMKMLAIFWNSTTIQDACLLOIFAHISLGMESTYLLAM 121
 QY 121 AFDRVAICHPLEAHATVLTLPRTKIGVAAVVRGAALMAPLPVPIKLPFCRSNIIISHSY 180
 DB 122 AFDRVAICHPLEAHATVLTLPRTKIGVAAVVRGAALMAPLPVPIKLPFCRSNIIISHSY 181
 QY 181 CLHODVMKLACDDIRVNVVYGLIYIISAGLSLISFSYLLIKTLYGLTREAOAKAFQ 240
 DB 182 CLHODVMKLACDDIRVNVVYGLIYIISAGLSLISFSYLLIKTLYGLTREAOAKAFQ 241
 QY 241 TCVSHVCAVFIFYPFIFGLSVHFRFSKRDSPLVLIANTLYLVPLPLNIYVGVTKKEI 300
 DB 242 TCVSHVCAVFIFYPFIFGLSVHFRFSKRDSPLVLIANTLYLVPLPLNIYVGVTKKEI 301
 QY 301 RQRIILRFHVATHASEP 317
 DB 302 RQRIILRFHVATHASEP 318
 RESULT 5
 ABB44533;
 ID ABB44533 standard; Protein; 318 AA.
 XX
 AC ABB44533;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human GPCR7a polypeptide SEQ ID NO 26.

XX
 KM Human; GPCR; G-coupled protein-receptor; cardiac; antiarteriosclerotic;
 KM anabolic; cytotactic; antiviral; gene therapy; cardiomyopathy; obesity;
 KM anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KM asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
 KM infection; human immunodeficiency virus; HIV.
 XX
 OS Homo sapiens.
 XX
 PN MO200174904-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10241.
 XX
 PR 31-MAR-2000; 2000US-193664P.
 PR 05-APR-2000; 2000US-194614P.
 PR 06-APR-2000; 2000US-195063P.
 PR 06-APR-2000; 2000US-195066P.
 PR 06-APR-2000; 2000US-195067P.
 PR 06-APR-2000; 2000US-195068P.
 PR 06-APR-2000; 2000US-195069P.
 PR 06-APR-2000; 2000US-195070P.
 PR 06-APR-2000; 2000US-195510P.
 PR 21-UTL-2000; 2000US-219855P.
 PR 27-UTL-2000; 2000US-221284P.
 PR 28-UTL-2000; 2000US-221325P.
 PR 11-AUG-2000; 2000US-224588P.
 PR 11-OCT-2000; 2000US-239613P.
 PR 18-JAN-2001; 2001US-262508P.
 PR 23-JAN-2001; 2001US-263433P.
 PR 23-JAN-2001; 2001US-263604P.
 PR 30-JAN-2001; 2001US-265161P.
 PR 29-MAR-2001; 2001US-0823172.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Majumder K, Vernet CM, Casman SJ, Wolenc AR, Spaderna SK,
 PI Padigaru M, Mishnu VS, Tchernev VT, Spyrek KA, Li L,
 PI Baungartner JC, Gusev VY;
 DR WPI; 2001-639231/73.
 DR N-PSDB; ABA81542.
 XX
 PT New human G-protein coupled receptor X, GPCRX, polypeptide useful in
 PT treatment or prevention of GPCRX associated disorders e.g.
 PT cardiomyopathy or atherosclerosis, and to screen for antagonists and
 PT agonists useful therapeutically.
 XX
 PS Claim 1; Page 55; 157pp; English.
 XX
 CC The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 CC encode G-coupled protein-receptor related polypeptides
 CC (ABA84532-ABA84543). The isolated polypeptide having a sequence differing
 CC by no more than 15 % of amino acid residues from one of 22 amino acid
 CC sequences (or mature forms of the sequences), fully defined in the
 CC specification and corresponding to human G-protein coupled receptor X
 CC (GPCRX) polypeptides. The polypeptides have potential cardiac,
 CC antiarteriosclerotic, anabolic, cytotactic and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCRX-associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC haematopoietic disorders, developmental diseases, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV)-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to

CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents
 CC modulating cellular polypeptide expression or activity, useful as
 CC antagonists and agonists in disease treatment.

XX Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 22; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDNNGESSATYFLLIGLPGLERAOFWLAFPLCSLYLAVLGNLTIIYVREHSIHEP 60
 DB 2 MVDNNGESSATYFLLIGLPGLERAOFWLAFPLCSLYLAVLGNLTIIYVREHSIHEP 61
 QY 61 MYFLCMISGIDILISTSMRPMALIFWENSTTIQFACLIQFAIHSLSGMESTVLLAM 120
 DB 62 MYFLCMISGIDILISTSMRPMALIFWENSTTIQFACLIQFAIHSLSGMESTVLLAM 121
 QY 121 AFDRYVAICHPRLRATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
 DB 122 AFDRYVAICHPRLRATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 181
 QY 181 CLHODVMKLAACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 240
 DB 182 CLHODVMKLAACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 241
 QY 241 TCVSHVCAVFIFFYVPIGLSMVHRFSKRKDSPLPVILANIYLLVPPVLPVYGVTKKEI 300
 DB 242 TCVSHVCAVFIFFYVPIGLSMVHRFSKRKDSPLPVILANIYLLVPPVLPVYGVTKKEI 301
 QY 301 RORILRLPHVATASEP 317
 DB 302 RORILRLPHVATASEP 318

RESULT 6
 AAU24561
 ID AAU24561 standard; Protein; 318 AA.

AC AAU24561;
 DT 18-DEC-2001 (first entry)
 DE Human olfactory receptor AOLFRA8.
 XX

KM Human, olfactory receptor; G protein-coupled receptor; GPCR; odorant;
 KM food additive; cosmetic; fragrance; pharmaceutical additive.
 XX

OS Homo sapiens.
 XX

WO200168805-A2.
 XX

PD 20-SEP-2001.
 XX

PF 13-MAR-2001; 2001MO-US07771.
 XX

PR 13-MAR-2000; 2000US-0188914.
 XX

PR 24-MAR-2000; 2000US-0192033.
 XX

PR 12-APR-2000; 2000US-0198474.
 XX

PR 24-APR-2000; 2000US-0199335.
 XX

PR 26-MAY-2000; 2000US-0207702.
 XX

PR 23-JUN-2000; 2000US-0213849.
 XX

PR 16-AUG-2000; 2000US-0226534.
 XX

PR 07-SEP-2000; 2000US-0230732.
 XX

PR 07-FEB-2001; 2001US-0266662.
 XX

PA (SENSO-) SENOMIX INC.
 XX

XX Zozulya S;
 XX

XX WPI; 2001-570867/64.
 XX

XX N-PSDB; AAS42254.
 DR

XX Nucleic acids encoding human olfactory G protein-coupled receptors.
 PR useful for screening for compounds involved in olfactory sensation,
 PR where the compounds can be used in the food, pharmaceutical and
 PR cosmetic industries to customise odours -

XX Claim 60; Page 103-104; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The ORs
 CC specifically recognise molecules, odorants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence is a human olfactory receptor of the
 CC invention.

XX Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 22; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDNNGESSATYFLLIGLPGLERAOFWLAFPLCSLYLAVLGNLTIIYVREHSIHEP 60
 DB 2 MVDNNGESSATYFLLIGLPGLERAOFWLAFPLCSLYLAVLGNLTIIYVREHSIHEP 61
 QY 61 MYFLCMISGIDILISTSMRPMALIFWENSTTIQFACLIQFAIHSLSGMESTVLLAM 120
 DB 62 MYFLCMISGIDILISTSMRPMALIFWENSTTIQFACLIQFAIHSLSGMESTVLLAM 121
 QY 121 AFDRYVAICHPRLRATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
 DB 122 AFDRYVAICHPRLRATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 181
 QY 181 CLHODVMKLAACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 240
 DB 182 CLHODVMKLAACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 241
 QY 241 TCVSHVCAVFIFFYVPIGLSMVHRFSKRKDSPLPVILANIYLLVPPVLPVYGVTKKEI 300
 DB 242 TCVSHVCAVFIFFYVPIGLSMVHRFSKRKDSPLPVILANIYLLVPPVLPVYGVTKKEI 301
 QY 301 RORILRLPHVATASEP 317
 DB 302 RORILRLPHVATASEP 318

RESULT 7

AAU01306
 ID AAU01306 standard; Protein; 318 AA.

AC AAU01306;
 DT 04-OCT-2001 (first entry)
 DE P835P amino acid sequence.
 XX

XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 XX cyclostatic; gene therapy; metastasis.
 XX

OS Homo sapiens.
 XX

WO200151633-A2.
 XX

PD 19-JUL-2001.
 XX

PF 16-JAN-2001; 2001MO-US01574.
 XX

PR 14-JAN-2000; 2000US-0483672.
 XX

CC their corresponding DNA molecules. GPCR is also referred as useful for
 CC transmembrane receptor. G protein-coupled receptor protein is useful for
 CC treating neurological disorder, particularly schizophrenia. GPCR protein
 CC is also useful for identifying compounds useful for treating
 CC schizophrenia. These compounds are also useful for treating other
 CC neurological and psychiatric diseases, e.g. depression, anxiety, bipolar
 CC disease, affective disorders, attention deficit hyperactivity disorder/
 CC attention deficit disorder, epilepsy, neuritis, neuroasthenia, neuropathy,
 CC neurosis, Alzheimer's disease, Parkinson's disease, migraine and senile
 CC dementia. The invention also provides genetic screening procedures that
 CC entail analysing a person's genome with respect to GPCR. The vectors are
 CC useful for the recombinant production of the GPCR's. The present sequence
 CC is human CON198 G protein-coupled receptor (GPCR) protein.

XX Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 22; Length 318;

Best Local Similarity 99.7%; Pred. No. 5.9e-169; Mismatches 0; Gaps 0;

Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDNNGESSATYFILLGLPGLAEQFWLAFPLCSLYLAVLGNLTIIYVTEHSLHEP 60

DB 2 MVDNNGESSATYFILLGLPGLAEQFWLAFPLCSLYLAVLGNLTIIYVTEHSLHEP 61

QY 61 MYFLCMLSGIDILISTSSMPKMLAFWENSTIQPDACILQFAHISLGMESTVLLAM 120

DB 62 MYFLCMLSGIDILISTSSMPKMLAFWENSTIQPDACILQFAHISLGMESTVLLAM 121

QY 121 AFDRYVAICHPRLHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSY 180

DB 122 AFDRYVAICHPRLHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSY 181

QY 181 CLHODVWKLACDDIRVNVVYGLIVISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 240

DB 182 CLHODVWKLACDDIRVNVVYGLIVISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 241

QY 241 TCVSHVCAVFIFFYPFGLSMVHRFSKRDSPLVILLANTYLLVPPVLPVYGVTKKEI 300

DB 242 TCVSHVCAVFIFFYPFGLSMVHRFSKRDSPLVILLANTYLLVPPVLPVYGVTKKEI 301

QY 301 RQRIIRLFHVATTHASEP 317

DB 302 RQRIIRLFHVATTHASEP 318

RESULT 9

AAAG71659 standard; Protein; 318 AA.

AC AAAG71659;

DT 30-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1340.

XX Human; olfactory receptor; OR; primary scent determination;

KM secondary scent determination; polypeptide library; odour receptor;

KW scent profile; scent fingerprint; scent representation.

XX Homo sapiens.

XX WO200127158-A2.

XX 19-APR-2001.

PF 06-OCT-2000; 2000MO-US27582.

PR 08-OCT-1999; 98US-0158615.

PR 24-FEB-2000; 2000US-0184809.

XX (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
 XX WPI: 2001-290713/30.
 DR
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 PS Claim 11; Page 826-827; 1857pp; English.

The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC facilities of different individuals.

XX Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 22; Length 318;

Best Local Similarity 99.7%; Pred. No. 5.9e-169; Mismatches 0; Gaps 0;

Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDNNGESSATYFILLGLPGLAEQFWLAFPLCSLYLAVLGNLTIIYVTEHSLHEP 60

DB 2 MVDNNGESSATYFILLGLPGLAEQFWLAFPLCSLYLAVLGNLTIIYVTEHSLHEP 61

QY 61 MYFLCMLSGIDILISTSSMPKMLAFWENSTIQPDACILQFAHISLGMESTVLLAM 120

DB 62 MYFLCMLSGIDILISTSSMPKMLAFWENSTIQPDACILQFAHISLGMESTVLLAM 121

QY 121 AFDRYVAICHPRLHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSY 180

DB 122 AFDRYVAICHPRLHATVLTLPRTKIGVAAVVRGALMAPLPVFIKQLPFCRSNLSHSY 181

QY 181 CLHODVWKLACDDIRVNVVYGLIVISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 240

DB 182 CLHODVWKLACDDIRVNVVYGLIVISAGLDSLLISFSYLLIKTVLGLTREAOAKAFG 241

QY 241 TCVSHVCAVFIFFYPFGLSMVHRFSKRDSPLVILLANTYLLVPPVLPVYGVTKKEI 300

DB 242 TCVSHVCAVFIFFYPFGLSMVHRFSKRDSPLVILLANTYLLVPPVLPVYGVTKKEI 301

QY 301 RQRIIRLFHVATTHASEP 317

DB 302 RQRIIRLFHVATTHASEP 318

RESULT 10

ABP95674 standard; Protein; 318 AA.

AC ABP95674;

DT 06-MAR-2003 (first entry)

DE Human GPCR polypeptide SEQ ID NO 158.

XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

KM drug development; gustatory; taste; fragrance; receptor.

XX Homo sapiens.

XX WO200216548-A2.

XX 28-FEB-2002.

XX

30-JUL-2001; 2001WO-IB01446.
 04-AUG-2000; 2000JP-0237818.
 13-FEB-2001; 2001JP-0034434.
 (NTSC-) JAPAN SCI & TECHNOLOGY CORP.
 Haga T, Takeda S, Mitaku S;
 WPI; 2002-304118/34.
 N-PSDB; AB242948.
 Database global search for G protein-coupled receptors, proteins and
 encoded genes for studying in vivo signal transduction mechanism and
 identifying targets for drug development
 Claim 10; SEQ ID NO 158; 97bp + Sequence Listing; Japanese.

The invention relates to a method for screening G protein-coupled
 receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins
 (AB243596-AB243942) by extracting open-reading frames containing 6-8
 transmembrane domains with 250-1000 amino acid residues to give a gene
 homologous with a known GPCR gene. The receptor proteins and encoded
 genes are useful for studying in vivo signal transduction mechanism and
 identifying targets for drug development e.g. based on olfactory and
 gustatory receptors in form of agonists and antagonists by screening
 intrinsic and extrinsic ligands as bitter taste inhibitors, taste
 enhancers and fragrance improvers.
 Note: The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pcr_sequences.

Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 23; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MVDPNGNSATYFLIGLPGLEAOPFLAPPLSLYLIVLGNLTIIYVREHSHEP 60
 2 MVDPNGNSATYFLIGLPGLEAOPFLAPPLSLYLIVLGNLTIIYVREHSHEP 61
 61 MYFLCMISGIDIIISTSSMPKMLAIWFNSTTIQPDACILQIPAHISGMESTVLLAM 120
 62 MYFLCMISGIDIIISTSSMPKMLAIWFNSTTIQPDACILQIPAHISGMESTVLLAM 121
 121 AFDRAVAICHPRLRAATVTLPRVTKIGVAAYVGAALMAPLPVFIKQLPCRSHVLSHSY 180
 122 AFDRAVAICHPRLRAATVTLPRVTKIGVAAYVGAALMAPLPVFIKQLPCRSHVLSHSY 181
 181 CLHODVMKLACDDIRVNVVGLIVISAIGLSLISFSYLLIKTVLGLTREAOAFAFG 240
 182 CLHODVMKLACDDIRVNVVGLIVISAIGLSLISFSYLLIKTVLGLTREAOAFAFG 241
 241 TCVSHVCAVFLFYVPIGSLSVHRFSKRRDSPVLIIANILVLPVLPNIYGVGVTKEI 300
 242 TCVSHVCAVFLFYVPIGSLSVHRFSKRRDSPVLIIANILVLPVLPNIYGVGVTKEI 301
 301 RQRILRLFHVAATHASEP 317
 302 RQRILRLFHVAATHASEP 318

RESULT 11

AB2435411 standard; Protein; 318 AA.

AB2435411;

19-JUL-2002 (first entry)

Human P835P protein SEQ ID NO 920.

Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
 gene therapy.
 Homo sapiens.
 US2002022248-A1.

21-FEB-2002.

12-JAN-2001; 2001US-0759143.

25-FEB-1997; 97US-0906099.
 01-AUG-1997; 97US-0904804.
 09-FEB-1998; 98US-0020956.
 25-FEB-1998; 98US-0030607.
 14-JUL-1998; 98US-0115453.
 23-SEP-1998; 98US-0159812.
 15-JAN-1999; 99US-0232149.
 09-APR-1999; 99US-0288946.
 13-JUL-1999; 99US-0352616.
 18-NOV-1999; 99US-0439313.
 14-JAN-2000; 2000US-0483672.
 27-MAR-2000; 2000US-0536857.
 09-MAY-2000; 2000US-0568100.
 12-MAY-2000; 2000US-0570737.
 13-JUN-2000; 2000US-0593793.
 27-JUN-2000; 2000US-0605783.
 10-AUG-2000; 2000US-0636215.
 29-AUG-2000; 2000US-0651236.
 06-SEP-2000; 2000US-0657279.
 02-OCT-2000; 2000US-0679426.
 10-OCT-2000; 2000US-0685166.

(XUJ/) XU J.
 (DILL/) DILLON D C.
 (MITC/) MITCHAM J L.
 (HARL/) HARLOCKER S L.
 (JIAN/) JIANG Y.
 (KALO/) KALOS M D.
 (FANG/) FANGER G R.
 (RETT/) RETTER M W.
 (STOL/) STOLK J A.
 (DAYC/) DAY C H.
 (VEDV/) VEDVICK T S.
 (CART/) CARTER D.
 (LISX/) LI S X.
 (WANG/) WANG A.
 (SKET/) SKELTY Y A W.
 (HEPL/) HEPLER W T.
 (HEND/) HENDERSON R A.
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 Li SX, Wang A, Skelty YAM, Hepler WT, Henderson RA;
 WPI; 2002-255649/30.

New prostate-specific polynucleotides for diagnosing and treating
 diseases, in particular prostate cancer, and as markers for the
 progression of cancer

Claim 2; SEQ ID NO 920; 87bp; English.

The present invention provides prostate-specific coding sequences and
 their encoded proteins. These can be used in the diagnosis and treatment
 of cancers, particularly prostate cancer. The present sequence is a
 protein described in the invention.

Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 23; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;

Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYDPNGNSSATYFLLIGLPGLEAOFWLAFLCSLYLIANVTGNTIIVYVTEHSHHP 60
 DB 2 MYDPNGNSSATYFLLIGLPGLEAOFWLAFLCSLYLIANVTGNTIIVYVTEHSHHP 61

QY 61 MYIFLCMISGIDILISTSMKPMKLAIFWNSSTIIOFACDLOIFAHSLSGNESTVLLAM 120
 DB 62 MYIFLCMISGIDILISTSMKPMKLAIFWNSSTIIOFACDLOIFAHSLSGNESTVLLAM 121

QY 121 AFDRYVAICHPLRHATVTLTPRVTKIGVAAYVRGAALMAPLPVFKOLPFCRSNLSHSY 180
 DB 122 AFDRYVAICHPLRHATVTLTPRVTKIGVAAYVRGAALMAPLPVFKOLPFCRSNLSHSY 181

QY 131 CHQDVWKLACDDIRVNVVYGLIYISAIGDLSLISFSYLLIKTYVGLTREAOAKAFG 240
 DB 182 CHQDVWKLACDDIRVNVVYGLIYISAIGDLSLISFSYLLIKTYVGLTREAOAKAFG 241

QY 241 TCVSHVCAVFIFYPFGLSMVHRFSKRDSPLPVILANIYLVPPVLPNPIYGVKTKXI 300
 DB 242 TCVSHVCAVFIFYPFGLSMVHRFSKRDSPLPVILANIYLVPPVLPNPIYGVKTKXI 301

QY 301 RORILRPHVATHASEP 317
 DB 302 RORILRPHVATHASEP 318

RESULT 12

AAU95746 standard; Protein; 318 AA.

AAU95746;
 02-JUN-2002 (first entry)

Human olfactory and pheromone G protein-coupled receptor #33.

Human; olfactory and pheromone G protein coupled; receptor;
 GPCR; transducer; antidepressant; neuroleptic; endocrine; anabolic;
 anorectic; taste; fragrance; food additive; cosmetic; cell migration;
 sterility; psychotic disorder; neurological disorder; anxiety;
 schizophrenia; manic depression; depression; axonal growth;
 menstrual cycle; appetite sexual motivation; sexual attraction;
 aggression.

KM
 OS Homo sapiens.
 XX
 PN WO200224726-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 21-SEP-2001; 2001WO-BE00162.
 XX
 PR 22-SEP-2000; 2000EP-0870211.
 XX
 PA (CHEM-) CHEMCOM SA.
 XX
 PI Velthen A;
 XX
 DR MPI: 2002-330013/36.
 XX
 DR N-PSDB; A8K68633.
 XX
 PT Novel pheromone G-protein coupled receptor and receptor-derived
 PT agonists, antagonists or inhibitors useful in food or cosmetic products
 PT or in the treatment or prevention of neurological disorders such as
 PT anxiety and schizophrenia -
 XX
 PS Disclosure; Page 710-711; 833pp; English.

CC The invention relates to olfactory and Pheromone G-protein coupled
 CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
 CC portion and its encoding polynucleotide. Also included are an agonist,
 CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector

CC comprising the polynucleotide, a cell transformed by the vector, a non-
 CC human mammal comprising a partial or total deletion of the polynucleotide
 CC encoding the receptor and screening (detection and possibly, recovering)
 CC of compounds which are known or not known to be agonist, antagonists or
 CC inhibitors of natural compounds to the GPCR. The receptor-derived
 CC agonists, antagonists, inhibitors or compounds are used as an
 CC improvement, elimination or substitution of an existing taste and/or a
 CC fragrance of (or in) the food and/or cosmetic products. They can also be
 CC used in the preparation of medication in the treatment and/or prevention
 CC of a mammalian disorder, such as cell migration, sterility, psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, depression, for promoting axonal growth, nerve cell
 CC connection and nerve regeneration for modulating male and female
 CC endocrine functions, hormone production and the menstrual cycle, for the
 CC prevention or the treatment by stimulation of several mammalian
 CC behaviours, such as stimulation or suppression of appetite, sexual
 CC motivation, sexual attraction, aggression and for promoting or
 CC suppressing chemical communication between organisms. The present
 CC sequence is a human olfactory and pheromone GPCR protein sequence.

Sequence 318 AA;

Query Match 99.8%; Score 1614; DB 23; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5.9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYDPNGNSSATYFLLIGLPGLEAOFWLAFLCSLYLIANVTGNTIIVYVTEHSHHP 60
 DB 2 MYDPNGNSSATYFLLIGLPGLEAOFWLAFLCSLYLIANVTGNTIIVYVTEHSHHP 61

QY 61 MYIFLCMISGIDILISTSMKPMKLAIFWNSSTIIOFACDLOIFAHSLSGNESTVLLAM 120
 DB 62 MYIFLCMISGIDILISTSMKPMKLAIFWNSSTIIOFACDLOIFAHSLSGNESTVLLAM 121

QY 121 AFDRYVAICHPLRHATVTLTPRVTKIGVAAYVRGAALMAPLPVFKOLPFCRSNLSHSY 180
 DB 122 AFDRYVAICHPLRHATVTLTPRVTKIGVAAYVRGAALMAPLPVFKOLPFCRSNLSHSY 181

QY 131 CHQDVWKLACDDIRVNVVYGLIYISAIGDLSLISFSYLLIKTYVGLTREAOAKAFG 240
 DB 182 CHQDVWKLACDDIRVNVVYGLIYISAIGDLSLISFSYLLIKTYVGLTREAOAKAFG 241

QY 241 TCVSHVCAVFIFYPFGLSMVHRFSKRDSPLPVILANIYLVPPVLPNPIYGVKTKXI 300
 DB 242 TCVSHVCAVFIFYPFGLSMVHRFSKRDSPLPVILANIYLVPPVLPNPIYGVKTKXI 301

QY 301 RORILRPHVATHASEP 317
 DB 302 RORILRPHVATHASEP 318

RESULT 13

AAU85181 standard; Protein; 318 AA.

AAU85181;
 08-MAY-2002 (first entry)

G-coupled olfactory receptor #42.

Human; olfactory G-coupled receptor; sensory perception of odourant;
 odour composition; taste composition.

KM
 OS Homo sapiens.
 XX
 PN WO200198526-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US20122.
 XX
 PR 22-JUN-2000; 2000US-213812P.

PR 13-MAR-2001; 2001US-0804291.
 XX (SENO-) SENOMYX INC.
 XX Zozulya S, Stryer L;
 XX WPI: 2002-083330/11.
 DR N-PSDB; ABK37540.
 PT Representing sensory perception of one or more odourants for the
 PT identification and design of tastes and odours comprises providing a
 PT representative group of n olfactory receptors -
 XX
 PS Claim 1; Page 77; 182pp; English.
 CC The invention relates to a method of representing sensory perception of
 CC one or more odourants. The method comprises: (a) providing a
 CC representative class of n olfactory receptors or ligand binding domains
 CC (LBD) of these receptors; (b) measuring values Xi to Xn representative
 CC of at least one activity of one or more odourants selected from:
 CC (i) binding one or more odourants to the LBD of at least one of the n
 CC olfactory receptors; (ii) activating at least one of the n
 CC olfactory receptors with the one or more odourants; and (iii) blocking at
 CC least one of the n olfactory receptors with the one or more odourants;
 CC and (c) generating a representation of sensory perception from the values
 CC Xi to Xn. The representation of the sensory perception of odourants is
 CC useful for the design and formulation of odour and taste compositions.
 CC AA085140-AA085393 represent human olfactory G-coupled receptor amino acid
 CC sequences of the invention.
 XX
 SQ Sequence 318 AA;
 Query Match 99.8%; Score 1614; DB 23; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5,9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPNGNESATYFILIGLPGLEAQPWLAFPLCSLYLAVAGNTLIYVTEHSLHP 60
 DB 2 MDPNGNESATYFILIGLPGLEAQPWLAFPLCSLYLAVAGNTLIYVTEHSLHP 61
 QY 61 MYFLCMLSGIDLLISTSSMPKMLAFWNSTTIQFDACLLQFAIHSLSGNESTVLLAM 120
 DB 62 MYFLCMLSGIDLLISTSSMPKMLAFWNSTTIQFDACLLQFAIHSLSGNESTVLLAM 121
 QY 121 AFDYVAICHPLRHATVLTLPRTKIGVAAVRGALMLAPVFKQLPFCRSNTLSHSY 180
 DB 122 AFDYVAICHPLRHATVLTLPRTKIGVAAVRGALMLAPVFKQLPFCRSNTLSHSY 181
 QY 181 CLHQDVWKACDDIRNVVYGLIVISAIGDLSLISPSYLLIKTVLGLTREAAKAFG 240
 DB 182 CLHQDVWKACDDIRNVVYGLIVISAIGDLSLISPSYLLIKTVLGLTREAAKAFG 241
 QY 241 TCVSHCAVEIFVFPFGISMTWRFSKRDSPPLVTLANTYLVLPVLPNTIYGVKTEI 300
 DB 242 TCVSHCAVEIFVFPFGISMTWRFSKRDSPPLVTLANTYLVLPVLPNTIYGVKTEI 301
 QY 301 RQRILRLFHVATRASFP 317
 DB 302 RQRILRLFHVATRASFP 318
 RESULT 14
 AB071842
 ID AB071842 standard; Protein; 318 AA.
 AC AB071842;
 XX 10-JUN-2003 (first entry)
 DT
 XX Prostate cancer associated protein #66.
 DE Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
 KW immunogen; cancer; prostate specific antigen; PSA;

KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
 KW PSMA.
 XX Homo sapiens.
 XX US2002192763-A1.
 XX 19-DEC-2002.
 XX 29-JUN-2001; 2001US-0895793.
 XX 17-APR-2000; 2000US-157455P.
 XX 04-OCT-2000; 2000US-0679272.
 XX 28-MAR-2001; 2001US-0822827.
 XX (XUJ/) XU J.
 XX (DILL/) DILLON D C.
 XX (MITC/) MITCHAM J L.
 XX (HARL/) HARLOCKER S L.
 XX (JIAN/) JIANG Y.
 XX (KALO/) KALOS M D.
 XX (FANG/) FANGER G R.
 XX (RETT/) RETTER M W.
 XX (STOL/) STOLK J A.
 XX (DAYC/) DAY C H.
 XX (VEDV/) VEDVICK T S.
 XX (CART/) CARTER D.
 XX (LISK/) LI S X.
 XX (WANG/) WANG A.
 XX (SKEI/) SKEIKY Y A W.
 XX (HEPL/) HEPLER W T.
 XX (HEND/) HENDERSON R A.
 XX (HURA/) HURAL J.
 XX (MCNE/) MCNETT P D.
 XX (HOUN/) HOUGHTON R L.
 XX (DEBA/) Y DE BAASOLS C V.
 XX (FOYT/) FOY T M.
 XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
 PI Mcnell PD, Houghton RL, Y De Baasols CV, Foy TM;
 DR WPI: 2003-352711/33.
 XX New fusion protein comprising prostate-specific polypeptides, or its
 PT immunogenic portions, useful for diagnosing, preventing and/or treating
 PT cancer, particularly prostate cancer -
 XX Example 15; SEQ ID NO 920; 85pp; English.
 XX The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 80 %
 CC sequence identity to any one of the 3 sequences defined in the USPTO
 CC web site, which is encoded by any of the 4 nucleotide sequences not
 CC defined in the specification. The fusion protein, composition and
 CC methods are useful for diagnosing, preventing and/or treating cancer,
 CC particularly prostate cancer. The proteins are useful as markers to
 CC indicate the presence or absence of cancer. This is the amino acid
 CC sequence of a prostate cancer therapy associated protein.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC seqdata.uspto.gov/sequence.html?DocID=US20020192763.
 XX
 SO Sequence 318 AA;
 Query Match 99.8%; Score 1614; DB 24; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5,9e-169;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDPNGNESATYFILIGLPGLEAQPWLAFPLCSLYLAVAGNTLIYVTEHSLHP 60

```

Db      2  MWDPNGNSSATYFLLIGLPGLEBAQFWLAPPLCSLYLAVLGNLTIIYVRETHSLHEP 61
Qy      61  MYIFLCMLSGDILISTSSMPKMLAIFWNSSTTIQFDACLLQIQAHSLSGMESTVLLAM 120
Db      62  MYIFLCMLSGDILISTSSMPKMLAIFWNSSTTIQFDACLLQIQAHSLSGMESTVLLAM 121
Qy      121  AFDSYVAICHPLRATVTLTFRVTKIGVAAYVRGAALMAPLPVFIKQLPFCRSNIISSHY 180
Db      122  AFDSYVAICHPLRATVTLTFRVTKIGVAAYVRGAALMAPLPVFIKQLPFCRSNIISSHY 181
Qy      181  CLHODVMTLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 240
Db      182  CLHODVMTLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 241
Qy      241  TCVSHVCVAFIFYPYFPGLSWHRFSSKRSDPLPVIIANTYLLVPPVLPNIYVGVTKKEI 300
Db      242  TCVSHVCVAFIFYPYFPGLSWHRFSSKRSDPLPVIIANTYLLVPPVLPNIYVGVTKKEI 301
Qy      301  RORILRFLFVATHASEP 317
Db      302  RORILRFLFVATHASEP 318

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RESULT 15
ABP81974
ID  ABP81974 standard; Protein, 318 AA.
AC  ABP81974;
DT  04-MAR-2003 (first entry)
DE  Human G protein-coupled receptor l653440 protein SEQ ID NO:434.

```

```

XX  G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM  G protein-coupled receptor modulator; antibody; immune-related disease;
KM  growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM  immunological-related cell proliferative disease; autoimmune disease;
KM  Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM  osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM  graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM  psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM  mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM  hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.

```

```

XX  Homo sapiens.
XX  W0200261087-A2.
XX  08-AUG-2002.
XX  19-DEC-2001; 2001WO-US50107.
XX  19-DEC-2000; 2000US-257144P.
XX  (LIFE-) LIFESPAN BIOSCIENCES INC.
XX  Burner GC, Roush CL, Brown JP;
XX  WPI; 2003-045718/04.
XX  N-PSDB; ABZ42822.

```

```

XX  New isolated antigenic peptides e.g., for G protein-coupled receptors
XX  (GPCR), useful for diagnosing and designing drugs for treating
XX  conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
XX  cancer or autoimmune diseases

```

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XX  Disclosure; Fig 1; 523pp; English.

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```

CC  The present invention describes antigenic peptides (I) comprising:
CC  (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC  acids. Also described: (1) an assay for the detection of a particular

```

```

CC  G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC  and (2) an isolated antibody having high specificity and high affinity
CC  or avidity for a particular GPCR. (1) can be used as GPCR modulators and
CC  in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC  an antibody against a particular GPCR, and in the production of specific
CC  antibodies. The peptides and antibodies are also useful for detecting the
CC  presence or absence of corresponding GPCRs. The antigenic peptides for
CC  GPCRs and antibodies are useful for diagnosing and designing drugs for
CC  treating immune-related diseases, growth-related diseases, cell
CC  regeneration-related disease, immunological-related cell proliferative
CC  diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC  atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC  osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC  inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC  disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC  anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC  loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC  hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC  any other disorder in which GPCRs are involved. The antibodies may be
CC  used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC  GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC  exemplification of the present invention.
XX
SQ  Sequence 318 AA:

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Query Match 99.8%; Score 1614; DB 24; Length 318;
Best Local Similarity 99.7%; Pred. No. 5.9e-163;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      2  MWDPNGNSSATYFLLIGLPGLEBAQFWLAPPLCSLYLAVLGNLTIIYVRETHSLHEP 61
Qy      61  MYIFLCMLSGDILISTSSMPKMLAIFWNSSTTIQFDACLLQIQAHSLSGMESTVLLAM 120
Db      62  MYIFLCMLSGDILISTSSMPKMLAIFWNSSTTIQFDACLLQIQAHSLSGMESTVLLAM 121
Qy      121  AFDSYVAICHPLRATVTLTFRVTKIGVAAYVRGAALMAPLPVFIKQLPFCRSNIISSHY 180
Db      122  AFDSYVAICHPLRATVTLTFRVTKIGVAAYVRGAALMAPLPVFIKQLPFCRSNIISSHY 181
Qy      181  CLHODVMTLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 240
Db      182  CLHODVMTLACDDIRVNVVYGLIYIISAIGDSLISFSYLLIKTYLGLTREAOAKAFG 241
Qy      241  TCVSHVCVAFIFYPYFPGLSWHRFSSKRSDPLPVIIANTYLLVPPVLPNIYVGVTKKEI 300
Db      242  TCVSHVCVAFIFYPYFPGLSWHRFSSKRSDPLPVIIANTYLLVPPVLPNIYVGVTKKEI 301
Qy      301  RORILRFLFVATHASEP 317
Db      302  RORILRFLFVATHASEP 318

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Search completed: February 9, 2004, 16:23:47
Job time : 44 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 16:05:17 ; Search time 797 Seconds
(without alignments)
10621.628 Million cell updates/sec

Title: US-10-017-066A-1

Perfect score: 3136
Sequence: 1 cagagagcgtctatttcagt.....aaaaaaaaaaaaaaaa 3136

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3136	100.0	3136	22	AAF83880
2	3136	100.0	3136	25	ABZ4822
3	2913.4	92.9	3104	24	ABK92202
4	2028.4	64.7	2061	22	AAH64175
5	2028.4	64.7	2061	22	AAH59393
6	2028.4	64.7	2061	22	AAH18119
7	2028.4	64.7	2061	24	ABL95546
8	2028.4	64.7	2061	25	ACA59983

9	1287.8	41.1	1302	21	AAA9351	G protein-coupled
10	1287.8	41.1	1302	22	AAH64174	Human prostate cDN
11	1287.8	41.1	1302	22	AAH93938	P835P full length
12	1287.8	41.1	1302	24	ABL95545	Human P835P cDNA s
13	1287.8	41.1	1302	25	ACA59982	Prostate cancer th
14	966.4	30.6	968	22	AAH81542	Human GPCR7a polyn
15	964.2	30.7	969	22	AAH81543	Human GPCR7b polyn
16	962.2	30.7	968	22	AAH81544	Human GPCR7c polyn
17	955.4	30.5	957	22	AAH64176	Human prostate cDN
18	955.4	30.5	957	22	AAH42254	Human CDNA encoding
19	955.4	30.5	957	22	AAH93940	P835P open reading
20	955.4	30.5	957	22	ADH06504	Human CON198 G pro
21	955.4	30.5	957	24	ABZ42948	Human GPCR polynuc
22	955.4	30.5	957	24	ABJ95547	Human P835P cDNA s
23	955.4	30.5	957	24	ABK68633	Human DNA for olfa
24	955.4	30.5	957	24	ABK37540	DNA encoding G-co
25	955.4	30.5	957	25	ACA59984	Prostate cancer th
26	952.4	30.4	954	22	AAH64177	Human prostate cDN
27	952.4	30.4	954	22	AAH93941	P835P open reading
28	952.4	30.4	954	22	AAH31835	Human olfactory re
29	952.4	30.4	954	24	ABJ95548	Human P835P cDNA s
30	952.4	30.4	954	25	ACA59985	Prostate cancer th
31	684.8	21.8	753	22	AAH07990	Human CDNA clone (
32	614.6	19.6	660	23	ABV20491	Human prostate exp
33	614.6	19.6	660	23	ABV23865	Human prostate exp
34	614.6	19.6	660	23	ABV26329	Human prostate exp
35	614.6	19.6	660	23	ABV29742	Human prostate exp
36	555.4	17.7	853	23	ABV22883	Human prostate exp
37	555.4	17.7	853	23	ABV28845	Human prostate exp
38	555.4	17.7	853	23	ABV23042	Human prostate exp
39	555.4	17.7	853	23	ABV24202	Human prostate exp
40	555.4	17.7	853	23	ABV25521	Human prostate exp
41	555.4	17.7	853	23	ABV28403	Human prostate exp
42	555.4	17.7	853	23	ABV28674	Human prostate exp
43	555.4	17.7	853	23	ABV28878	Human prostate exp
44	488.8	15.6	504	23	ABV15654	Human prostate exp
45	488.8	15.6	593	23	ABV37135	Human prostate exp

ALIGNMENTS

RESULT 1	
AAF83880	
ID	AAF83880 standard; cDNA; 3136 BP.
XX	
AC	AAF83880;
XX	
DT	06-AUG-2001 (first entry)
XX	
DE	Human G-protein coupled receptor, PHOR-1 encoding cDNA.
XX	
KW	G-protein-coupled receptor; prostate; cancer; PHOR-1; kidney; uterine;
KW	cervical; stomach; rectal; cytostatic; vaccine; cell function regulator;
KW	human; prostate homologue of olfactory receptor-1; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key Location/Qualifiers
FT	CDS 133..1086
FT	/tag= a
FT	/product= "PHOR-1"
XX	
PN	WO200125434-A1.
XX	
PD	12-APR-2001.
XX	
PF	05-OCT-2000; 2000MO-US27543.
XX	
PR	05-OCT-1999; 99US-0157902.
XX	
PA	(UROC-) UROGENESYS INC.
XX	

[illegible]


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QY 1681 TATGACCCCTGTTTCTTATTTATTTCTTATCAACCCCTTAAATTAGCCAAAGATTT 1740
DB 1681 TATGACCCCTGTTTCTTATTTATTTCTTATCAACCCCTTAAATTAGCCAAAGATTT 1740
QY 1741 ATTATGACCCCTGTTTCTTATTTATTTCTTATCAACCCCTTAAATTAGCCAAAGATTT 1800
DB 1741 ATTATGACCCCTGTTTCTTATTTATTTCTTATCAACCCCTTAAATTAGCCAAAGATTT 1800
QY 1801 TGGGGTCATACAGATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860
DB 1801 TGGGGTCATACAGATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1860
QY 1861 TGGGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
DB 1861 TGGGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1921 ATTTCCTAGAGAGAGATTTAAATTTCTTCTCATCTCATCCAGTGTGATTTAGAAATTC 1980
DB 1921 ATTTCCTAGAGAGAGATTTAAATTTCTTCTCATCTCATCCAGTGTGATTTAGAAATTC 1980
QY 1981 CTGGGCAACAGAACTCATGCTTTAATCCACTAGCTATTTGCTTATTTGCTGCTCAATT 2040
DB 1981 CTGGGCAACAGAACTCATGCTTTAATCCACTAGCTATTTGCTTATTTGCTGCTCAATT 2040
QY 2041 GCCAATTACCTGTGCTTGGAGAGAGATTTCTAGGTTCAACCATATAGAGAAATCTTA 2100
DB 2041 GCCAATTACCTGTGCTTGGAGAGAGATTTCTAGGTTCAACCATATAGAGAAATCTTA 2100
QY 2101 TTGAGAAAGCTGTGATAGAGAGCTTATAGCAAGTATTTAATTTTAAAGTTCCATAGTGA 2160
DB 2101 TTGAGAAAGCTGTGATAGAGAGCTTATAGCAAGTATTTAATTTTAAAGTTCCATAGTGA 2160
QY 2161 TTCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
DB 2161 TTCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
QY 2221 TCTTGAAGATTAACATTTGGCCTTTTGAAGTGTGACTGTAGCTGAAAGTGAAGGAACTTTC 2280
DB 2221 TCTTGAAGATTAACATTTGGCCTTTTGAAGTGTGACTGTAGCTGAAAGTGAAGGAACTTTC 2280
QY 2281 AGGACCAATGCTTTATTTGGGGCTTTGTGTGAGATGAAACAGGAACTTTGAGACCAAGAA 2340
DB 2281 AGGACCAATGCTTTATTTGGGGCTTTGTGTGAGATGAAACAGGAACTTTGAGACCAAGAA 2340
QY 2341 GCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
DB 2341 GCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
QY 2401 TTAATAGGTTTCACTTCAACAGATATGACAAACAGTGTAAACCAAGAACTCAAAATTAC 2460
DB 2401 TTAATAGGTTTCACTTCAACAGATATGACAAACAGTGTAAACCAAGAACTCAAAATTAC 2460
QY 2461 AAATCTAAAAAGATGATGATATATATATATATATATATATATATATATATATATATATAT 2520
DB 2461 AAATCTAAAAAGATGATGATATATATATATATATATATATATATATATATATATATAT 2520
QY 2521 TTCCCTGATATGATTTCCCTAATAACAGTGTTCATCCCTTTTGTATATGATATATATAT 2580
DB 2521 TTCCCTGATATGATTTCCCTAATAACAGTGTTCATCCCTTTTGTATATGATATATATAT 2580
QY 2581 GGAATAGCTATATATATATATATATATATATATATATATATATATATATATATATATAT 2640
DB 2581 GGAATAGCTATATATATATATATATATATATATATATATATATATATATATATATATAT 2640
QY 2641 TATATATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2700
DB 2641 TATATATGATATATATATATATATATATATATATATATATATATATATATATATATATAT 2700
QY 2701 AGCAAAAGTCCCTAGAGACATATATATATATATATATATATATATATATATATATATAT 2760
DB 2701 AGCAAAAGTCCCTAGAGACATATATATATATATATATATATATATATATATATATATAT 2760
QY 2761 TGAATCTCTGTCTGAGAGACATATATATATATATATATATATATATATATATATATATAT 2820

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DB 2761 TGAATCTCTGTCTGAGAGACATATATATATATATATATATATATATATATATATATATAT 2820
QY 2821 TTAATTAATCTGAGCAATTAATCTTCAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
DB 2821 TTAATTAATCTGAGCAATTAATCTTCAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 CTGGCTCATTAACCCCTCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
DB 2881 CTGGCTCATTAACCCCTCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
QY 2941 AGCTATGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
DB 2941 AGCTATGCTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000
QY 3001 GCCAAACCTCTGTCAATTTGCAATCCCACTTGTATTTGTATGAGAGAGAGAGAGAGAGAG 3060
DB 3001 GCCAAACCTCTGTCAATTTGCAATCCCACTTGTATTTGTATGAGAGAGAGAGAGAGAGAG 3060
QY 3061 AAATTAAGTACTATTTGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
DB 3061 AAATTAAGTACTATTTGTGTGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120
QY 3121 AAAAAAAAAAAAAA 3136
DB 3121 AAAAAAAAAAAAAA 3136

RESULT 2
AB242822
ID AB242822 standard; DNA; 3136 BP.
XX
AC AB242822;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor Le53440 nucleotide SEQ ID NO:433.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor; modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related disease; cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN NC0200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001NC-0550107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PI (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP,
XX
DR WPI; 2003-046718/04.
XX
PT P-PSDB; ABP81974.
XX
PS New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Disclosure; Fig 1; 523pp; English.

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Db      1800 TGGGGTCATACAGTATATAAATT--AAAAAAAAAGACTTCAGCCCATCTCATATGA 1857
QY      1861 TGTGAAGAACTGTAGAGAGAACCAAGGGTAGGGGTAGAGATTTCCAGAGCTTTAC 1920
Db      1858 TGTGAAGAACTGTAAAGAGACCAAGGGTAGGGGTAGAGATTTCCAGAGCTTTAC 1917
QY      1921 ATTTCAGAGAGGATTTTATTTCTCTCATCTACAGTGTCTATTTAGAAATTTG 1980
Db      1918 ATTTCATAGAGAGATTTTATTTCTCTCATCTACAGTGTGTATTTAGAAATTTG 1977
QY      1981 CTGGCAACAGAGCTATGCTTTTATCCCACTAGTATTTGTTATGCTGTCCTCAATT 2040
Db      1978 CTGGCAACAGAGCTATGCTTTTATCCCACTAGTATTTGTTATGCTGTCCTCAATT 2037
QY      2041 GCCAATTACTGTGTCTTGAAGAGAGTATTTAGGTTACCATTTAGGAAGATTTCTTA 2100
Db      2038 GCCAATTACTGTGTCTTGAAGAGAGTATTTAGGTTACCATTTAGGAAGATTTCTTA 2097
QY      2101 TTGAGAAAGCTGTGATGAGGCTTATAGCAAGTATTTTATTTTAAAGTTCCATAGTGA 2160
Db      2098 TTGAGAAAGCTGTGATGAGGCTTATAGCAAGTATTTTATTTTAAAGTTCCATAGTGT 2157
QY      2161 TTCTGATAGGCACTGAGGTTAGGAGCCACAGTTATGATGGAGATATGGAATGGCAGG 2220
Db      2158 TTCTGATAGGCACTGAGGTTAGGAGCCACAGTTATGATGGAGATATGGAATGGCAGG 2217
QY      2221 TCTTGAAGATACATGAGCCTTTTGAAGTGTGATCTGATCTGGAAGTGAAGGAACTTTC 2280
Db      2218 TGTGGAAGATACATGAGCCTTTTGAAGTGTGATCTGATCTGGAAGTGAAGGAACTTTC 2277
QY      2281 AGGACCACTGCTTATTTGGGGCTTTTGTGAGATAGGACAGGACCTTTGAGACAGAGAA 2340
Db      2278 AGGACCACTGCTTATTTGGGGCTTTTGTGAGATAGGAACTTTGAGACCGGAGAA 2337
QY      2341 GCATCTGACTTGGCATGGGAATCAGGCAATTTTCTTCTGAGGGGCTATTTACCAAGGG 2400
Db      2338 GCAATCTGACTTGGCATGGGAATCAGGCAATTTTCTTCTGAGGGGCTATTTACCAAGGG 2397
QY      2401 TTATAGGTTTCACTCTTCAACAGAGATATGACAAAGTGTAAACCAAGAACTCAATTAC 2460
Db      2398 TTATAGGTTTCACTCTTCAACAGAGATATGACAAAGTGTAAACCAAGAACTCAATTAC 2457
QY      2461 AAATCTAAACATGTGATCATATATGTGTGAAGTTTCAATTTCTTTTCAATCTCAGG 2520
Db      2458 AATCTACTAAACATGTGATCATATATGTGTGAAGTTTCAATTTCTTTTCAATCTCAGG 2517
QY      2521 TTCCCTGATATGGATCTATACATGCTTATGATCCCTTTTGTATGATGATATCATATT 2580
Db      2518 TTCCCTGATATGGATCTATACATGCTTATGATCCCTTTTGTATGATGATATCATATT 2577
QY      2581 GGAATGCTTATTTATCTTGTATTTGCTGTGACCTGTAAAGCCCATGAGGCACTGT 2640
Db      2578 GGAATGCTTATTTATCTTGTATTTGCTGTGACCTGTAAAGCCCATGAGGCACTGT 2637
QY      2641 TATATTTGAATGCTATCTCTGTTCATCATGACTGTCTTTTGTCTATCATTAATCCCC 2700
Db      2638 TATATTTGAATGCTATCTCTGTTCATCATGACTGTCTTTTGTCTATCATTAATCCCC 2697
QY      2701 AGCAAGTGTGAGATATATGCTTATGCTTATGACACCGGTTATTTTATCATCAAAAC 2760
Db      2698 AGCAAGTGTGAGATATATGCTTATGCTTATGACACCGGTTATTTTATCATCAAAAC 2757
QY      2761 TGATTTCTTCTGTCTGAAACACATAGCAGGCAATTTTCCAGCCTTTCTTTGAGTGGGTA 2820
Db      2758 TGATTTCTTCTGTCTGAAACACATAGCAGGCAATTTTCCAGCCTTTCTTTGAGTGGGTA 2817
QY      2821 TTATTAATTTCTGGCATTACTTCCATGATGATGAGTGAAGTGAATGTCATATTTCTATAC 2880
Db      2818 TTATTAATTTTATGCAATTTACTTCCATGATGATGAGTGAAGTGAATTTTATATAC 2877
QY      2881 CTGGCTCATTAACCTCTCCCATGTGAGGCTTTCAATGTTGACATTAATGTGACTTGGGA 2940
Db      2878 CTGGCTCATTAACCTCTCCCATGTGAGGCTTTCAATGTTGACATTAATGTGACTTGGGA 2937

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QY      2941 AGCTATGTTTACACAGAGTAAATCACC 2968
Db      2938 AGCTATGTTTACACAGAGTAAATTAAC 2965

RESULT 4
AAS64175
ID      AAS64175 standard; cDNA; 2061 BP.
XX
AC      AAS64175;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Human prostate cDNA sequence #594.
XX
KW      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS      Homo sapiens.
XX
PN      WO200173032-A2.
XX
PD      04-OCT-2001.
XX
PF      27-MAR-2001; 2001WO-US0919.
XX
PR      27-MAR-2000; 2000US-0536857.
PR      09-MAY-2000; 2000US-0568100.
PR      12-MAY-2000; 2000US-0570737.
PR      13-JUN-2000; 2000US-0593793.
PR      27-JUN-2000; 2000US-0605783.
PR      10-AUG-2000; 2000US-0636215.
PR      29-AUG-2000; 2000US-0651236.
PR      06-SEP-2000; 2000US-0657279.
PR      02-OCT-2000; 2000US-0679426.
PR      10-OCT-2000; 2000US-0685166.
XX
PA      (CORI-) CORIXA CORP.
XX
PI      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI      Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick RS, Carter D;
PI      Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
XX
DR      WPI; 2001-639232/73.
XX
PT      New human prostate-specific polypeptides and polynucleotides useful for
PT      the diagnosis and treatment of cancer, especially prostate cancer -
PS      Claim 1; Page 566-567; 579pp; English.
XX
CC      The invention relates to isolated prostate-specific
CC      polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC      antibodies raised against the polypeptides (or antigenic epitopes
CC      derived from them) and antigen-presenting cells expressing the
CC      polypeptides. The antibodies are useful for detecting the presence of
CC      cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC      the antigen-presenting cells are useful for stimulating and/or expanding
CC      T cells specific for a tumour protein, and for inhibiting the development
CC      of cancer especially prostate cancer. Compositions comprising the
CC      polynucleotide and/or polypeptide are useful for stimulating an immune
CC      response, and for treating cancer. The oligonucleotide is useful for
CC      detecting cancer. The present sequence is a prostate specific
CC      polynucleotide of the invention.
XX
SQ      Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;

Query Match      64.7%; Score 2028.4; DB 22; Length 2061;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY      1029 GATTGACAGCGGATCTTGTGACTTTTCATGTGGCCACAGCGCTTCAGAGCCCTAGGT 1088
Db      3 GATTGACAGCGGATCTTGTGACTTTTCATGTGGCCACAGCGCTTCAGAGCCCTAGGT 62

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QY 1089 GTCACTGATCAAACTCTTTTCCATTCAGAGTCTCTGATTCAGATTTTATGTTAAT 1148
 Db 63 GTCACTGATCAAACTCTTTTCCATTCAGAGTCTCTGATTCAGATTTTATGTTAAT 122
 QY 1149 TTTGGAAACAGATATTCGAAAAAAATTTCTTTAATAAAAATACACTCAGATCTTC 1208
 Db 123 TTTGGAAACAGATATTCGAAAAAAATTTCTTTAAT--AAAAATACACTCAGATCTTC 181
 QY 1209 AAAATGAAACTGGTTGGGGAATCTCCATTTTTCATATATATTTCTCTTGTCTTC 1268
 Db 182 AAAATGAAACTGGTTGGGGAATCTCCATTTTTCATATATATTTCTCTTGTCTTC 241
 QY 1269 TGTCAATATAATTAATAAACCCTGACTAGTGTGGTTGGAGGTTATTAATCTTTCA 1328
 Db 242 TGTCAATATAATTAATAAACCCTGACTAGTGTGGTTGGAGGTTATTAATCTTTCA 301
 QY 1329 TTTACCATGAGTCCAAATCTAAACTGTTCTACTGATGTTTACAGATTCAGATTA 1388
 Db 302 TTTACCATGAGTCCAAATCTAAACTGTTCTACTGATGTTTACAGATTCAGATTA 361
 QY 1389 GAATGATCATCTAGAGAACATTTGCCAAAGGCTTAAGCAAGGCAAGAAAAATTAAC 1448
 Db 362 GAATGATCATCTAGAGAACATTTGCCAAAGGCTTAAGCAAGGCAAGAAAAATTAAC 421
 QY 1449 AGAATATAATTAATGAGATATCTAGTTAAATCTAATACTTCTTCAAGATCTCCA 1508
 Db 422 AGAATATAATTAATGAGATATCTAGTTAAATCTAATACTTCTTCAAGATCTCCA 481
 QY 1509 ACCACATGATCTCAGAAAAATGCTGCTCAAAATGACTCTTACAGAGAAAAATTAAT 1568
 Db 482 ACCACATGATCTCAGAAAAATGCTGCTCAAAATGACTCTTACAGAGAAAAATTAAT 541
 QY 1569 TTTTCTCTGAGCACTAGCACTTAAGGGGAAGATTTGAGATAAGCCTTGAAGAATAC 1628
 Db 542 TTTTCTCTGAGCACTAGCACTTAAGGGGAAGATTTGAGATAAGCCTTGAAGAATAC 601
 QY 1629 AATTACCTAGTATTAAGTTGACACACTGTTCTGAGAGTTTTCACAGCAATGAGACC 1688
 Db 602 AATTACCTAGTATTAAGTTGACACACTGTTCTGAGAGTTTTCACAGCAATGAGACC 661
 QY 1689 CTGTTTTCCTAATTAATTTCTATCACTTAACTTATTTAGGCAAGATTTTATAGTAC 1748
 Db 662 CTGTTTTCCTAATTAATTTCTATCACTTAACTTATTTAGGCAAGATTTTATAGTAC 721
 QY 1749 CCTATCTGAGCCATGAGAAAAATGATGTTCACTGGGGGATCACTGAATTAATGAGGCTCA 1808
 Db 722 CCTATCTGAGCCATGAGAAAAATGATGTTCACTGGGGGATCACTGAATTAATGAGGCTCA 781
 QY 1809 TACAAGTATAAAATTTAAAAAAAAGACTTCATGCCCAATCTCATATGATGAGAAAG 1868
 Db 782 TACAAGTATAAAATTT--AAAAAAAAGACTTCATGCCCAATCTCATATGATGAGAAAG 839
 QY 1869 AACTGTTAGAGACCAACAGGGTAGTGGTTAGAGATTTTCAGAGTCTTCAATTTTCTA 1928
 Db 840 AACTGTTAGAGACCAACAGGGTAGTGGTTAGAGATTTTCAGAGTCTTCAATTTTCTA 899
 QY 1929 GAGAGGATTAATTTCTCTCATCTCATCCAGGTTGTTTAAAGAAATTTCTGAGCAAC 1988
 Db 900 GAGAGGATTAATTTCTCTCATCTCATCCAGGTTGTTTAAAGAAATTTCTGAGCAAC 959
 QY 1989 AGAACTCATGCTTTAATCCACATGCTATGCTTATGTCCTGATCCAAATGCGCAATTA 2048
 Db 960 AGAACTCATGCTTTAATCCACATGCTATGCTTATGTCCTGATCCAAATGCGCAATTA 2048
 QY 2049 CCTGCTCTTGAAGAGAGATTTCTAGGTTCACTATAGAAAGATTTCTTATTCAGAAA 2108
 Db 1020 CCTGCTCTTGAAGAGAGATTTCTAGGTTCACTATAGAAAGATTTCTTATTCAGAAA 2108
 QY 2109 GTCTGATAGAGGCTTATAGCAAGTTATTTTAAAGTTCCATAGGTTGATCTGATA 2168
 Db 1080 GTCTGATAGAGGCTTATAGCAAGTTATTTTAAAGTTCCATAGGTTGATCTGATA 2168

QY 2169 GGCAGTAGAGTTAGGGAGCCACAGTTATGATGGGAAGATTAAGATGAGAGTCTTGAAG 2228
 Db 1140 GGCAGTAGAGTTAGGGAGCCACAGTTATGATGGGAAGATTAAGATGAGAGTCTTGAAG 1199
 QY 2229 ATTAATGAGCTTTTGAAGTGAATCTGAGTGGAAAGTGAAGGAATCTTCAAGACCAT 2288
 Db 1200 ATTAATGAGCTTTTGAAGTGAATCTGAGTGGAAAGTGAAGGAATCTTCAAGACCAT 1259
 QY 2289 GCTTTATTTGGGGCTTTTGAAGTGAATGGAACAGGAACTTTGAGACCAAGAAAGCAATCTG 2348
 Db 1260 GCTTTATTTGGGGCTTTTGAAGTGAATGGAACAGGAACTTTGAGACCAAGAAAGCAATCTG 1319
 QY 2349 ACTTAGGATGGAATTCAGGCAATTTTCTCTGAGGGGCTATTAACAAAGGTTAATAGG 2408
 Db 1320 ACTTAGGATGGAATTCAGGCAATTTTCTCTGAGGGGCTATTAACAAAGGTTAATAGG 1379
 QY 2409 TTTCACTTTCAACAGAGATTAACAAAGTGTAAACAAAGAACTCAATTAACAAATCTA 2468
 Db 1380 TTTCACTTTCAACAGAGATTAACAAAGTGTAAACAAAGAACTCAATTAACAAATCTA 1439
 QY 2469 AAACATGATCATATATGTTGAGTGAATTTCAATTTCTTTCAATCCCTCAGGTTCCCTGA 2528
 Db 1440 AAACATGATCATATATGTTGAGTGAATTTCAATTTCTTTCAATCCCTCAGGTTCCCTGA 1499
 QY 2529 TATGATTTCTTAATACATGCTTTCAATCCCTTTTGTAAAGATTAATTAATGATC 2588
 Db 1500 TATGATTTCTTAATACATGCTTTCAATCCCTTTTGTAAAGATTAATTAATGATC 1559
 QY 2589 CTATTTAATCTGATTTGTTGCTGCTGAGCTTAAGCCATTAAGGCACTGTTTATATG 2648
 Db 1560 CTATTTAATCTGATTTGTTGCTGCTGAGCTTAAGCCATTAAGGCACTGTTTATATG 1619
 QY 2649 AATGATCTCTGTTCACTATGACTGCTCTTCTCATCACTTAATCCCTCAGGAAAGT 2708
 Db 1620 AATGATCTCTGTTCACTATGACTGCTCTTCTCATCACTTAATCCCTCAGGAAAGT 1679
 QY 2709 GCTTGAACATTAATGCTGTTATGCTTGAACACCGGTTATTTTATCAAACTGATTCCT 2768
 Db 1680 GCTTGAACATTAATGCTGTTATGCTTGAACACCGGTTATTTTATCAAACTGATTCCT 1739
 QY 2769 TCTGCTGGAACATATAGCCAGGCAATTTTCCAGCCTTCTGAGTTGGGATTAATTA 2828
 Db 1740 TCTGCTGGAACATATAGCCAGGCAATTTTCCAGCCTTCTGAGTTGGGATTAATTA 1799
 QY 2829 TTTGGCCATTAATCTTCAATGATGAGTGAAGTGAATGCAATTTCTAATCTGAGCTCA 2888
 Db 1800 TTTGGCCATTAATCTTCAATGATGAGTGAAGTGAATGCAATTTCTAATCTGAGCTCA 1859
 QY 2889 TAAAACCTCCCATGATGAGGCTTCAATGTTGATTAATTAATGATGAGGAACTATGCT 2948
 Db 1860 TAAAACCTCCCATGATGAGGCTTCAATGTTGATTAATTAATGATGAGGAACTATGCT 1919
 QY 2949 GTTACACAGATTAATCAACAGAAAGCTGATTTCTGAAAAAACTGTGCAAGGCAAAAC 3008
 Db 1920 GTTACACAGATTAATCAACAGAAAGCTGATTTCTGAAAAAACTGTGCAAGGCAAAAC 1979
 QY 3009 TCTGCTATTTGCACTCCCACTTGTATTTGTAGCAAGGAGTTGATTAAGTAAAAATTA 3068
 Db 1980 TCTGCTATTTGCACTCCCACTTGTATTTGTAGCAAGGAGTTGATTAAGTAAAAATTA 2039
 QY 3069 GTACTATTTGTCAAG 3084
 Db 2040 GTACTATTTGTCAAG 2055

RESULT 5
 AAH93939 standard, cDNA, 2061 BP.
 ID AAH93939
 AC AAH93939;
 XX
 DT 04-OCT-2001 (first entry)
 XX

DE FLJ13581 cDNA sequence.
XX Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytostatic; gene therapy; metastasis; ss.
XX Homo sapiens.
XX MO200151633-A2.
XX 19-JUL-2001.
XX 16-JAN-2001; 2001WO-US01574.
XX 14-JAN-2000; 2000US-0483672.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky VM;
PI Wang A, Mesgher MJ;
XX WPI; 2001-425873/45.
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
XX Claim 1; Page 532-533; 543pp; English.
XX
XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;
SQ
Query Match 64.7%; Score 2028.4; DB 22; Length 2061;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
QY 1029 GATTGACAGCGCATCTTCGACCTTTCATGTCGACACACAGCTTCAGAGCCCTAGT 1088
DB 3 GATTGACAGCGCATCTTCGACCTTTCATGTCGACACACAGCTTCAGAGCCCTAGT 62
QY 1089 GTCAGGATCAACTCTTTCATTCAGAGTCTTCGATTCAGATTTTAAATGTTAAAT 1148
DB 63 GTCAGGATCAACTCTTTCATTCAGAGTCTTCGATTCAGATTTTAAATGTTAAAT 122
QY 1149 TTTGAGACAGTATTCAGAAAAAAATTTCTTAAATAAAAAATCACTAGATCTTC 1208
DB 123 TTTGAGACAGTATTCAGAAAAAAATTTCTTAAATAAAAAATCACTAGATCTTC 181
QY 1209 AAATATGAACGTGTGGGAAATTCACATTTTCAATATATTTCTTCTTGTTCCT 1268
DB 182 AAATATGAACGTGTGGGAAATTCACATTTTCAATATATTTCTTCTTGTTCCT 241
QY 1269 TGTCTACATTAATTAATTAATCCCTGACATGATGTTGGTGAAGGTTAATACCTTCAT 1388
DB 242 TGTCTACATTAATTAATTAATCCCTGACATGATGTTGGTGAAGGTTAATACCTTCAT 301
QY 1329 TTTACCATGACATGCAATATGAACATGCTTCTACTGATGTTTACAGCATTCAGATAA 1388
DB 302 TTTACCATGACATGCAATATGAACATGCTTCTACTGATGTTTACAGCATTCAGATAA 361

QY 1389 GAATGATACATCTAGAGAACATTTGCCAAAAGGCTTAGACACGGCAAGAAATTAACAC 1448
DB 362 GAATGATACATCTAGAGAACATTTGCCAAAAGGCTTAGACACGGCAAGAAATTAACAC 421
QY 1449 AGAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1508
DB 422 AGAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 481
QY 1509 ACCAATTGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCAACAGAGAAATTAAT 1568
DB 482 ACCAATTGATCTCAGAAAAATGCTGTCTTCAAAATGACTTCAACAGAGAAATTAAT 541
QY 1569 TTTTCTCTGGAACATAGCACTTAAGGGAAGATGGAAGTAAAGCTTGAAGAGTAC 1628
DB 542 TTTTCTCTGGAACATAGCACTTAAGGGAAGATGGAAGTAAAGCTTGAAGAGTAC 601
QY 1629 ATTACCTAGCTTAATGAAGATGACACACTGTCTGAGAGTTTCAACAGCATATGAGAC 1688
DB 602 ATTACCTAGCTTAATGAAGATGACACACTGTCTGAGAGTTTCAACAGCATATGAGAC 661
QY 1689 CTGTTTCTCTTAATTAATTTCTTATCAACCTTATTAATGAGCAAGATTAATTAAT 1748
DB 662 CTGTTTCTCTTAATTAATTTCTTATCAACCTTATTAATGAGCAAGATTAATTAAT 721
QY 1749 CCTCATGTCAGCAATGAGAAATTAATGTTCACTGAGGATCACTGAATTAATGAGGCTCA 1808
DB 722 CCTCATGTCAGCAATGAGAAATTAATGTTCACTGAGGATCACTGAATTAATGAGGCTCA 781
QY 1809 TACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1868
DB 782 TACAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 839
QY 1869 AACTGTTAGAGACCAACACAGGATGAGGTTAGAGATTTCCAGATCTTAATTTCTTA 1928
DB 840 AACTGTTAGAGACCAACACAGGATGAGGTTAGAGATTTCCAGATCTTAATTTCTTA 899
QY 1929 GAGAGGATTAATTAATTTCTTCACTCACTCACTGTTGATTAAGAAATTTCTGCAAC 1988
DB 900 GAGAGGATTAATTAATTTCTTCACTCACTCACTGTTGATTAAGAAATTTCTGCAAC 959
QY 1989 AGAATCTAGCTTATATCCACTAGCTATGCTTAATGCTGATCCAAATTA 2048
DB 960 AGAATCTAGCTTATATCCACTAGCTATGCTTAATGCTGATCCAAATTA 1019
QY 2049 CCTGATCTGGAAGAAAGATTTCTTCACTCACTCACTGTTGATTAAGAAATTTCTGCAAC 2108
DB 1020 CCTGATCTGGAAGAAAGATTTCTTCACTCACTCACTGTTGATTAAGAAATTTCTGCAAC 1079
QY 2109 GTCGATAGGCTTATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2168
DB 1080 GTCGATAGGCTTATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1139
QY 2169 GGCAGTGAAGTTAGGAGACCAACAGTTATGATGGAAGATGAGCAAGCTTGAAG 2228
DB 1140 GGCAGTGAAGTTAGGAGACCAACAGTTATGATGGAAGATGAGCAAGCTTGAAG 1199
QY 2229 ATAACTAGGCTTATGAGTGAATCTGAGTGAAGGAGGATCTTCAAGACAT 2288
DB 1200 ATAACTAGGCTTATGAGTGAATCTGAGTGAAGGAGGATCTTCAAGACAT 1259
QY 2289 GCTTATTTGGGCTTGTGACATATGAAACAGGACCTTGAACACAGAAACAAATCTG 2348
DB 1260 GCTTATTTGGGCTTGTGACATATGAAACAGGACCTTGAACACAGAAACAAATCTG 1319
QY 2349 ACTTAGGATGGAATCAGGCAATTTTGTCTGAGAGGCTTATCAAGAGGTTAATAG 2408
DB 1320 ACTTAGGATGGAATCAGGCAATTTTGTCTGAGAGGCTTATCAAGAGGTTAATAG 1379
QY 2409 TTTCACTTCAACAGATATGACACAGTGTAAACCAAGAAATCAATTAACAAATACTA 2468
DB 1380 TTTCACTTCAACAGATATGACACAGTGTAAACCAAGAAATCAATTAACAAATACTA 1439

QY 2469 AAACATGATCATATAATGAGTATGATTTCTTTTCTTTTCAATCTCTAGTTCCTCTA 2528
 DB 1440 AAACATGATCATATAATGAGTATGATTTCTTTTCTTTTCAATCTCTAGTTCCTCTA 1499
 QY 2529 TATGATTCCTATAACATGCTTTTCAATCTCTTTTGTAAATGATATCATATTTGAAATGC 2588
 DB 1500 TATGATTCCTATAACATGCTTTTCAATCTCTTTTGTAAATGATATCATATTTGAAATGC 1559
 QY 2589 CTATTTATATCTGATTTGCTGTGACCTGTAAAGCCCAAGAGGCACTGTTATATTTG 2648
 DB 1560 CTATTTATATCTGATTTGCTGTGACCTGTAAAGCCCAAGAGGCACTGTTATATTTG 1619
 QY 2649 AATGTCATCTGTCATCATATGATCTGCTTTGCTCATATGAAATCCCAAGAAAGT 2708
 DB 1620 AATGTCATCTGTCATCATATGATCTGCTTTGCTCATATGAAATCCCAAGAAAGT 1679
 QY 2709 GCTTAAACATTAATGAGTATGCTTATGCTGACACCGGTTATTTTCAATCAAACTGATTCCT 2768
 DB 1680 GCTTAAACATTAATGAGTATGCTTATGCTGACACCGGTTATTTTCAATCAAACTGATTCCT 1739
 QY 2769 TCTGTCTGAAACATATGACCCAGCAATTTTCAAGCCTTTGAGTTGGTATTTATTA 2828
 DB 1740 TCTGTCTGAAACATATGACCCAGCAATTTTCAAGCCTTTGAGTTGGTATTTATTA 1799
 QY 2829 TTTGCGCATTAATCTTCAATGATGAGTGAAGTGAATGCAATTTCTATACCTGCTCA 2888
 DB 1800 TTTGCGCATTAATCTTCAATGATGAGTGAAGTGAATGCAATTTCTATACCTGCTCA 1859
 QY 2889 TAAACCTCCATGACAGCTTCTTCAATGATGAGTGAAGTGAATGCAATTTCTATACCTGCTCA 2948
 DB 1860 TAAACCTCCATGACAGCTTCTTCAATGATGAGTGAAGTGAATGCAATTTCTATACCTGCTCA 1919
 QY 2949 GTTACACAGATTAATACACAGAGCTGATTTCTGAAAAAACTGTGACAGCCAAAC 3008
 DB 1920 GTTACACAGATTAATACACAGAGCTGATTTCTGAAAAAACTGTGACAGCCAAAC 1979
 QY 3009 TCTGTCTGAAACATATGACCCAGCAATTTTCAAGCCTTTGAGTTGGTATTTATTA 3068
 DB 1980 TCTGTCTGAAACATATGACCCAGCAATTTTCAAGCCTTTGAGTTGGTATTTATTA 2039
 QY 3069 GTACTATTTGTCTAG 3084
 DB 2040 GTACTATTTGTCTAG 2055
 RESULT 6
 AAH1819
 ID AAH1819 standard; cDNA; 2061 BP.
 AC AAH1819;
 DT 26-JUN-2001 (first entry)
 DE Human cDNA sequence SEQ ID NO:17984.
 KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 XX EPI074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JF-0248036.
 XX 27-AUG-1999; 99JF-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 03-JUN-2000; 2000JP-0241899.
 PA (HELI-) HELIX RES INST.
 XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-118749/34.
 DR
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 PS
 PS
 PS Claim 8; SEQ ID 17984; 2537bp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH1628 and
 CC AAH35833 represent human cDNA sequences; AAB92446 to
 CC AAH35833 represent human amino acid sequences; and AAH1629 to AAH1632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

SQ Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;

Query Match 64.7%; Score 2028.4; DB 22; Length 2061;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

QY 1029 GATTGACAGGCGACCTTTCATGCTTTCATGAGGCAACAGGCTTCAAGCCCTAGT 1088
 DB 3 GATTGACAGGCGACCTTTCATGCTTTCATGAGGCAACAGGCTTCAAGCCCTAGT 62
 QY 1089 GTCAATGATCAATCTTTTCCATTCAGAGTCTCTGATTCAGATTTTAAATGTTAAT 1148
 DB 63 GTCAATGATCAATCTTTTCCATTCAGAGTCTCTGATTCAGATTTTAAATGTTAAT 122
 QY 1149 TTGGAAGACAGTATTCAGAAAAAAATTTCTTAAATAAAAATACAACTCAGATCCTTC 1208
 DB 123 TTGGAAGACAGTATTCAGAAAAAAATTTCTTAAATAAAAATACAACTCAGATCCTTC 181
 QY 1209 AAATATGAACCTGTTGGGGAATCTCCATTTTTCATATATATTTTCTTGTGTTCT 1268
 DB 182 AAATATGAACCTGTTGGGGAATCTCCATTTTTCATATATATTTTCTTGTGTTCT 241
 QY 1269 TGCTACATATATATTAATACCTGACTAGTGTGTTGAGAGGTTATTAATCTTTCAT 1328
 DB 242 TGCTACATATATATTAATACCTGACTAGTGTGTTGAGAGGTTATTAATCTTTCAT 301
 QY 1329 TTTACCATGCAATGCAATTTAAATCTGCTTCTAATGTTTAAACAGATTTGAGATTA 1388
 DB 302 TTTACCATGCAATGCAATTTAAATCTGCTTCTAATGTTTAAACAGATTTGAGATTA 361
 QY 1389 GAATGATACATCTAGAGAACATTTGGCAAGGCTTAAAGCAAGCAAGAAATTAACAC 1448
 DB 362 GAATGATACATCTAGAGAACATTTGGCAAGGCTTAAAGCAAGCAAGAAATTAACAC 421
 QY 1449 AGAATATATTAATGAATATCTAGCTTAAATCTTCTCTTCTTCAAGATCTCCA 1508
 DB 422 AGAATATATTAATGAATATCTAGCTTAAATCTTCTCTTCTTCAAGATCTCCA 481

[illegible]

PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 (XUJ/) XU J.
 (DILL/) DILLON D C.
 (MITC/) MITCHAM J L.
 (HARL/) HARLOCKER S L.
 (JIAN/) JIANG Y.
 (KALO/) KALOS M D.
 (FANG/) FANGER G R.
 (RETT/) RETTER M W.
 (STOL/) STOLK J A.
 (DAYC/) DAY C H.
 (VEDV/) VEDVICK T S.
 (CART/) CARTER D.
 (LISK/) LI S X.
 (WANG/) WANG A.
 (SKEI/) SKEIKY Y A W.
 (HEPL/) HEPLER M T.
 (HEND/) HENDERSON R A.
 XX
 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler MT, Henderson RA;
 XX
 WPI: 2002-255649/30.
 XX
 New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer
 XX
 PS Claim 1; SEQ ID NO 917; 87pp; English.
 CC
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 CC
 CC Sequence 2061 BP; 612 A; 383 C; 399 G; 667 T; 0 other;
 SQ
 Query Match 64.7%; Score 2028.4; DB 24; Length 2061;
 Basic Local Similarity 99.8%; Pred. No. 0;
 Matches 2052; Conservative 0; Mismatches 1; Indels 3; Gaps 2;
 QY 1029 GATTCGACAGGCGATCCCTTGCATCTTTCAGAGTGGCCACACAGGCTTCAGAGCCCTAGGT 1088
 DB 3 GATTCGACAGGCGATCCCTTGCATCTTTCAGAGTGGCCACACAGGCTTCAGAGCCCTAGGT 62
 QY 1089 GTCAGTGATCAACTCTTTCATCAGAGTCTCTGATTCAGATTTTATGTAACT 1148
 DB 63 GTCAGTGATCAACTCTTTCATCAGAGTCTCTGATTCAGATTTTATGTAACT 122
 QY 1149 TTGGAAGACAGCTTTCAGAAAATAATTTCTTAATAAATAATCACTCAATCTCTTC 1208
 DB 123 TTGGAAGACAGCTTTCAGAAAATAATTTCTTAATAAATAATCACTCAATCTCTTC 181
 QY 1209 AATATGAACTGGTGGGGAATCTCAATTTTTCATATTTCTTCTTGTGTTTCT 1268
 DB 182 AATATGAACTGGTGGGGAATCTCAATTTTTCATATTTCTTCTTGTGTTTCT 241
 QY 1269 TGTCACTATATATTAATTAACCTGACCTGCTGCTGGTGGAGGTTATTAATCTTTCAT 1328
 DB 242 TGTCACTATATATTAATTAACCTGACCTGCTGCTGGTGGAGGTTATTAATCTTTCAT 301
 QY 1329 TTACACATGACATCAATCTAAACTGCTCTACTGATGGTTACAGCAATTCAGATA 1388
 DB 302 TTACACATGACATCAATCTAAACTGCTCTACTGATGGTTACAGCAATTCAGATA 361
 QY 1389 GAATGTACATCTTAGAGACATTTGCCAAGGCTTAAGCAGGCAAGAAATAAACAAC 1448

DB 362 GAATGTACATCTTAGAGACATTTGCCAAGGCTTAAGCAGGCAAGAAATAAACAAC 421
 QY 1449 AGAATATATTAATAAGATGATTAATCTAGCTTAATTAATCTCTCTTCAGAACTCCCA 1508
 DB 422 AGAATATATTAATAAGATGATTAATCTAGCTTAATTAATCTCTCTTCAGAACTCCCA 481
 QY 1509 ACCACATGGAGTCTGAGAAAATGCTGTCTTCAAAATGACTCTTCAGAGAAATAAT 1568
 DB 482 ACCACATGGAGTCTGAGAAAATGCTGTCTTCAAAATGACTCTTCAGAGAAATAAT 541
 QY 1569 TTTTCTCTGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCTTGAAGAGATAC 1628
 DB 542 TTTTCTCTGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCTTGAAGAGATAC 601
 QY 1629 ATTACCTAGCTTAATGAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGACC 1688
 DB 602 ATTACCTAGCTTAATGAAGTTGACACACTGTTCTGAGAGTTTTCACAGCATATGACC 661
 QY 1689 CTGTTTCTCTAATTAATTTCTTATCAACCTTTAATTAAGCAAGATTAATTAAGTAC 1748
 DB 662 CTGTTTCTCTAATTAATTTCTTATCAACCTTTAATTAAGCAAGATTAATTAAGTAC 721
 QY 1749 CCTCATTTGACCATGGGAAATGATGTCAGTGGGATCAGTGAATTAATGGGATCA 1808
 DB 722 CCTCATTTGACCATGGGAAATGATGTCAGTGGGATCAGTGAATTAATGGGATCA 781
 QY 1809 TACAAGTATTAATAATTAATAAAGATTCATGCCCATCTCATATGATGTGGAAG 1868
 DB 782 TACAAGTATTAATAATTAATAAAGATTCATGCCCATCTCATATGATGTGGAAG 839
 QY 1869 AACTGTAGAGAGACCAACAGGGTAGTGGTGTAGAGATTTCCAGAGCTTACATTTCTCA 1928
 DB 840 AACTGTAGAGAGACCAACAGGGTAGTGGTGTAGAGATTTCCAGAGCTTACATTTCTCA 899
 QY 1929 GAGAGGATTAATTTCTTCTCACTCATCAAGTGTGTATTAAGAAATTTCTGCGAAC 1988
 DB 900 GAGAGGATTAATTTCTTCTCACTCATCAAGTGTGTATTAAGAAATTTCTGCGAAC 959
 QY 1989 AGAATCATGGTCTTAATCCACATGATGATGCTATGCTGCTGCTGCTGCTGCTGCTGCT 2048
 DB 960 AGAATCATGGTCTTAATCCACATGATGATGCTATGCTGCTGCTGCTGCTGCTGCTGCT 1019
 QY 2049 CCTGTGCTTGAAGAGATGATTTCTAGTTCACCATTAAGAAATTTCTTATCAGAAA 2108
 DB 1020 CCTGTGCTTGAAGAGATGATTTCTAGTTCACCATTAAGAAATTTCTTATCAGAAA 1079
 QY 2109 GTCGCAATAGGCTTAATGCAAGTATTTATTTTAAAGTTCCATAGGTGATCTGATA 2168
 DB 1080 GTCGCAATAGGCTTAATGCAAGTATTTATTTTAAAGTTCCATAGGTGATCTGATA 1139
 QY 2169 GGCAGTGAAGTTAAGGACCAAGATTATGATGGAAGTATGATGAGCAAGTCTTGAAG 2228
 DB 1140 GGCAGTGAAGTTAAGGACCAAGATTATGATGGAAGTATGATGAGCAAGTCTTGAAG 1139
 QY 2229 AATAATTTGCTTTTGAAGTGAATGCTGATGCTGGAAGTGAAGGAATCTTCAGACCAT 2288
 DB 1200 AATAATTTGCTTTTGAAGTGAATGCTGATGCTGGAAGTGAAGGAATCTTCAGACCAT 1259
 QY 2289 GCTTATTTGGGGCTTTGTGAGATGATGAACAGGGAATTTGAGACCGAGAAAGCAATCTG 2348
 DB 1260 GCTTATTTGGGGCTTTGTGAGATGATGAACAGGGAATTTGAGACCGAGAAAGCAATCTG 1319
 QY 2349 ACTTAGCATGGGAATCAAGGATTTTCTTGAAGGGGCTATTACCAAGGGTTAATAGG 2408
 DB 1320 ACTTAGCATGGGAATCAAGGATTTTCTTGAAGGGGCTATTACCAAGGGTTAATAGG 1379
 QY 2409 TTTCATCTTCAACGAGATATGACACAGGTGTAACCAAGAACTCAATTAATCAATCTA 2468
 DB 1380 TTTCATCTTCAACGAGATATGACACAGGTGTAACCAAGAACTCAATTAATCAATCTA 1439
 QY 2469 AAACATGATCATATATGATGTAAGTTTCTTTTCAATCTCAGGTCTCCCTGA 2528

RESULT	B
ACAS59983	
ID	ACA59983 standard; cDNA; 2061 BP.
XX	
AC	ACA59983;
XX	
DT	10-JUN-2003 (first entry)
XX	
DE	Prostate cancer therapy associated cDNA #664.
XX	
KM	Prostate cancer; vaccine; gene therapy; cytosolic; fusion protein;
KM	immunogen; cancer; prostate specific antigen; PSA;
KM	prostatic acid phosphatase; PAP; prostate specific membrane antigen
XX	PSMA; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	US2002192763-A1.
XX	
PD	19-DEC-2002.
XX	
PF	29-JUN-2001; 2001US-0895793.
XX	
FR	17-APR-2000; 2000US-157455P.
PR	04-OCT-2000; 2000US-0679272.
PR	28-MAR-2001; 2001US-0822827.
XX	
PA	(XUUT/) XU J.
PA	(DILN/) DILON D C.
PA	(MITC/) MITCHAM J L.

Query Match	Best Local Similarity	Matches 2052; Conservative	Score 2028.4; 99.8%;	DB 25; Pred. No. 0;	Length 2061;	Mismatches 1;	Indels 3;	Gaps 2;
1029	GATTCGACAGGAGCCCTTCGACCTTTCCATGTGCGCCACACACGCTTCAGAGCCCTAGT	3	GATTCGACAGGAGCCCTTCGACCTTTCCATGTGCGCCACACACGCTTCAGAGCCCTAGT	62				
1089	GTCAGTATCAAACTTTCTTTCCATTCAGAGTCCCTGTGATTCAATTTAAATGTTAACAT	63	GTCAGTATCAAACTTTCTTTCCATTCAGAGTCCCTGTGATTCAATTTAAATGTTAACAT	1148				
1149	TTTGGAAGACAGTATTCAGAAAAAAATTTCTTAATTAATAAATAACAGCTAGATCCCTTC	123	TTTGGAAGACAGTATTCAGAAAAAAATTTCTTAATTAATAAATAACAGCTAGATCCCTTC	1208				
1209	AAATATGAAAATCGTTGGGAAATCTCCATTTTTCATATATATTTCTCTTGGTCTTTC	182	AAATATGAAAATCGTTGGGAAATCTCCATTTTTCATATATATTTCTCTTGGTCTTTC	1268				
1269	TGCTACATATATATATATATACCTGACTGAGTGTGGTGGAGGGTATATACCTTTTCAT	242	TGCTACATATATATATATATACCTGACTGAGTGTGGTGGAGGGTATATACCTTTTCAT	1328				

PD 13-APR-2000.
 XX 06-OCT-1999; 99WO-US23317.
 XX 06-OCT-1998; 98US-0167219.
 PR 06-OCT-1998; 98US-0172211.
 PR 11-MAY-1999; 99US-0133585.
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Yee H, Lal P, Bandman O, Au-cung J, Reddy R, Corley NC,
 PI Guegler KJ, Gorgone GA, Baughn MR, Azimzal Y,
 XX MPI; 2000-328934/28.
 DR P-PSDB; AAY92365.
 XX
 PT Novel human G-protein coupled receptor proteins used in the diagnosis,
 PT treatment and prevention of nervous system disorders,
 PT autoimmune/inflammatory disorders, and cell proliferative disorders
 PT such as cancer
 XX
 PS Claim 9; Page 78; 84pp; English.
 XX
 CC This sequence encodes human G-protein coupled receptor protein (GCRP) 5.
 CC The GCRP polypeptides, polynucleotides, antibodies, antagonists and
 CC agonists may be administered to human patients for the diagnosis,
 CC treatment and prevention of nervous system disorders (e.g. epilepsy,
 CC stroke, neoplasms, Alzheimer's disease), autoimmune or
 CC inflammatory disorders, complications of cancer, hemodialysis and
 CC extracorporeal circulation, and cell proliferative disorders. They are
 CC also used to treat or prevent disorders associated with decreased or
 CC increased expression or activity of GCRP.
 XX
 SQ Sequence 1302 BP; 277 A; 346 C; 259 G; 420 T; 0 other;
 XX
 Query Match 41.1%; Score 1287.8; DB 21; Length 1302;
 Best Local Similarity 99.8%; Pred. No. 4,4e-257;
 Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 XX
 QY 52 TGGACAAAGGGGTCACACATTCCTTCATACGAGTGAAGCTCTACCTGCTGTGCTGG 111
 Db 1 TGGACAAAGGGGTCACACATTCCTTCATACGAGTGAAGCTCTACCTGCTGTGCTGG 60
 QY 112 TCACATTTAGCTTCTTCATGATGATGATCCCAATGGCAATGAATCCAGTGTACATAC 171
 Db 61 TCACATTTAGCTTCTTCATGATGATGATCCCAATGGCAATGAATCCAGTGTACATAC 120
 QY 172 TTCATCTTAATAGGCTCCCTGATTTAGAGAGGCTCACTGCTGCTGCTGCTGCTGCTG 231
 Db 121 TTCATCTTAATAGGCTCCCTGATTTAGAGAGGCTCACTGCTGCTGCTGCTGCTGCTG 180
 QY 232 TGTCTCTTACCTTAATGCTGTGTAGTAACTTGACATCATATGATGCTGCTGCTGCTG 291
 Db 181 TGTCTCTTACCTTAATGCTGTGTAGTAACTTGACATCATATGATGCTGCTGCTGCTG 240
 QY 292 GAGCAGAGCTGATGAGAGGCTCAATATATTTCTTCAGCTTTGAGGATGACATC 351
 Db 241 GAGCAGAGCTGATGAGAGGCTCAATATATTTCTTCAGCTTTGAGGATGACATC 300
 QY 352 CTCATCTCCACTCAATCCATGCCCCAAATGCTGAGCATCTTGCTGATTAATTCACATAC 411
 Db 301 CTCATCTCCACTCAATCCATGCCCCAAATGCTGAGCATCTTGCTGATTAATTCACATAC 360
 QY 412 ATCCAGTTGATGCTGTGTGTGTAAGATTTTGGCATCACTGCTTAATTCAGATGAA 471
 Db 361 ATCCAGTTGATGCTGTGTGTGTAAGATTTTGGCATCACTGCTTAATTCAGATGAA 420
 QY 472 TCACAGTGTGCTGAGCATGCTTTTGAACGCTATGAGCATGTGAGCATGTGACCACTGGGC 531
 Db 421 TCACAGTGTGCTGAGCATGCTTTTGAACGCTATGAGCATGTGAGCATGTGACCACTGGGC 480
 QY 532 CATGCAAGTACTTAACTGCTGTGTGTGTCACCAAAATGTGTGTGTGTGTGTGTGTGTGT 591

Db 481 CATGCAAGTACTTAACTGCTGTGTGTGTGTCACCAAAATGTGTGTGTGTGTGTGTGTGTGT 540
 QY 592 GGGGTGACATGATGAGCAACCCCTTCTGTCTTCAATCAAGAGCTGCCCTTGTGCGCTGC 651
 Db 541 GGGGTGACATGATGAGCAACCCCTTCTGTCTTCAATCAAGAGCTGCCCTTGTGCGCTGC 600
 QY 652 AATATCTTTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 711
 Db 601 AATATCTTTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 660
 QY 712 ATCCGGTCAATGCTGT 771
 Db 661 ATCCGGTCAATGCTGT 720
 QY 772 CTTCATCT 831
 Db 721 CTTCATCT 780
 QY 832 GCCCAGGCAAGGATTTGGCACTTGGCTCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
 Db 781 GCCCAGGCAAGGATTTGGCACTTGGCTCTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 892 GTACCTTTCAATGATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 951
 Db 841 GTACCTTTCAATGATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 900
 QY 952 CCCCTCATCTTTGGCAATCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1011
 Db 901 CCCCTCATCTTTGGCAATCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
 QY 1012 GGAATGAAACAAAGAGATTTGCAACAGCGATCTTTCATGTCATGTCATGTCATGTCATGTCAT 1071
 Db 961 GGAATGAAACAAAGAGATTTGCAACAGCGATCTTTCATGTCATGTCATGTCATGTCATGTCAT 1020
 QY 1072 GCTTCAGAGCCCTTGAAGT 1131
 Db 1021 GCTTCAGAGCCCTTGAAGT 1080
 QY 1132 GATTTTAAATGTTAAATTTTGAAGACAGATTCAGAAAAAATTTCTTAATAAAAA 1191
 Db 1081 GATTTTAAATGTTAAATTTTGAAGACAGATTCAGAAAAAATTTCTTAATAAAAA 1139
 QY 1192 TACAACCTAGATCTTCAATTAATAAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1251
 Db 1140 TACAACCTAGATCTTCAATTAATAAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1199
 QY 1252 TTTCTTCTTTTGT 1311
 Db 1200 TTTCTTCTTTTGT 1259
 QY 1312 GGGTAAATCTTTCAATTTTACATGAGTCCAAATCTAAACT 1354
 Db 1260 GGGTAAATCTTTCAATTTTACATGAGTCCAAATCTAAACT 1302
 XX
 RESULT 10
 ID AAS64174 standard; cDNA; 1302 BP.
 XX
 AC AAS64174;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA sequence #593.
 XX
 KM Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 FN W0200173032-A2.
 XX
 PD 04-OCT-2001.
 XX

PF 27-MAR-2001; 2001WO-US09919.
 XX 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX

(CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
 PI Panzer GR, Reltter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 DR MPI; 2001-639232/73.
 XX P-PSDB; AA069951.

PT New human prostate-specific polypeptides and polynucleotides useful for
 XX the diagnosis and treatment of cancer, especially prostate cancer -
 XX Claim 1; Page 566; 579p; English.

XX The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumor protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.

SQ Sequence 1302 BP; 277 A; 346 C; 259 G; 420 T; 0 other;

Query Match 41.1%; Score 1287.8; DB 22; Length 1302;
 Best Local Similarity 99.8%; Pred. No. 4.4e-257;
 Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 52 TGGACAAAGGGGGTCAACATTCCTCCATAGGCTTGAAGCTTACCTGCTGCTG 111
 DB 1 TGGACAAAGGGGGTCAACATTCCTCCATAGGCTTGAAGCTTACCTGCTGCTG 60
 QY 112 TCAAGTTCAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 171
 DB 61 TCAAGTTCAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 172 TTCACTCAATAGGCTTCTGCTTGAAGAGGCTAGTTCGTGGCTTCCCATG 231
 DB 121 TTCACTCAATAGGCTTCTGCTTGAAGAGGCTAGTTCGTGGCTTCCCATG 180
 QY 232 TGGTCCCTTACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 291
 DB 181 TGGTCCCTTACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 292 GAGCAGAGCTGATGAGCCATGATATATTTCTTGCATGCTTTCAGGATGATG 351
 DB 241 GAGCAGAGCTGATGAGCCATGATATATTTCTTGCATGCTTTCAGGATGATG 300
 QY 352 CTCATTCAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 411
 DB 301 CTCATTCAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 QY 412 ATCCAGTTGATGCTTGTCTGCTACAGATTTTGCATGCTTTCATGCTGATGAA 471

DB 361 ATCCAGTTGATGCTTGTCTGCTACAGATGTTGCCATGCACTCTTATCTGGATGAA 420
 QY 472 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 531
 DB 421 TCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 532 CAGCCAGTACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
 DB 481 CAGCCAGTACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 592 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 651
 DB 541 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 652 AATATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711
 DB 601 AATATCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 712 ATCCGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 771
 DB 661 ATCCGAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 772 CTTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 831
 DB 721 CTTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 832 GCCCAGGCAAGGATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
 DB 781 GCCCAGGCAAGGATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 892 GTACCTTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
 DB 841 GTACCTTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 952 CCGCTCATCTTGGCAATATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
 DB 901 CCGCTCATCTTGGCAATATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 1012 GGAATGAAAGCAAGAGATTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
 DB 961 GGAATGAAAGCAAGAGATTTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 QY 1072 GCTTCAGAGGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131
 DB 1021 GCTTCAGAGGCTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 QY 1132 GATTTATGTTAATCAATTTGGAAGCAGTATTCAGAAAAAATTTCTTAAT 1191
 DB 1081 GATTTATGTTAATCAATTTGGAAGCAGTATTCAGAAAAAATTTCTTAAT 1139
 QY 1192 TCAACTCAGATGCTTCAATTAAGAACTGTTGGGAATTCATTTTCAATTAAT 1251
 DB 1140 TCAACTCAGATGCTTCAATTAAGAACTGTTGGGAATTCATTTTCAATTAAT 1199
 QY 1252 TTTCTTCTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1311
 DB 1200 TTTCTTCTTGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259
 QY 1312 GGGTTATTAATTTCAATTTTACATGAGTCAAGTCAATTAAT 1354
 DB 1260 GGGTTATTAATTTCAATTTTACATGAGTCAAGTCAATTAAT 1302

RESULT 11
 AAH93938
 ID AAH93938 standard; cDNA, 1302 BP.
 XX
 AC AAH93938;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE P835P full length cDNA sequence.
 XX

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
XX US200202248-A1.

XX 21-FEB-2002.
PD 12-JAN-2001; 2001US-0759143.

XX 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-015453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0558100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679428.
PR 10-OCT-2000; 2000US-0685166.

XX (XUJ)/ XU J.
PA (DILLON) DILLON D C.
PA (MITCHELL) MITCHELL J L.
PA (HARLOCKER) HARLOCKER S L.
PA (UTAN) UTAN Y.
PA (KALOS) KALOS M D.
PA (FANGER) FANGER G R.
PA (RETT) RETT M W.
PA (STOLK) STOLK J A.
PA (DAYC) DAY C H.
PA (VEDVICK) VEDVICK T S.
PA (CARTER) CARTER D.
PA (LISX) LI S X.
PA (WANG) WANG A.
PA (SKEIKY) SKEIKY Y A W.
PA (HEPLER) HEPLER W T.
PA (HENDERSON) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.

PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer

PS Claim 1; SEQ ID NO 916; 87bp; English.

XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.

XX Sequence 1302 Bf; 277 A; 346 C; 259 G; 420 T; 0 other;

Query Match 41.1%; Score 1287.8; DB 24; Length 1302;

Best Local Similarity 99.8%; Pred. No. 4.4e-257;
Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 52 TGGACAAAGGGGGTCAACATTCCTTCATACGATTGAGCCCTCACTGCTGCTGCG 111
Db 1 TGGACAAAGGGGGTCAACATTCCTTCATACGATTGAGCCCTCACTGCTGCTGCG 60
QY 112 TCACAGTTCAAGTCTTCATATGATGATGATGATGATGATGATGATGATGATGAT 171
Db 61 TCACAGTTCAAGTCTTCATATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 172 TTCATCTTAATAGGCTCCCTGCTTTAGAGAGGCTCACTTGGTGGCTTCCCATG 231
Db 121 TTCATCTTAATAGGCTCCCTGCTTTAGAGAGGCTCACTTGGTGGCTTCCCATG 180
QY 232 TGTCTCCCTTACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 291
Db 181 TGTCTCCCTTACCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 292 GAGCAGAGCTGATGAGGCGCATGATATATTTCTTGCATGCTTTCAGGATGACATC 351
Db 241 GAGCAGAGCTGATGAGGCGCATGATATATTTCTTGCATGCTTTCAGGATGACATC 300
QY 352 CTCATCTCCACTCATTCATGCGCCAAATGCTGGCATCTTCTGATTCATTCACATACC 411
Db 301 CTCATCTCCACTCATTCATGCGCCAAATGCTGGCATCTTCTGATTCATTCACATACC 360
QY 412 ATCCAGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 471
Db 361 ATCCAGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 472 TCACAGTGTGCTGCGCCATGCTTTTGAACCGCTATGAGGCTATGCTGACCCACTGCG 531
Db 421 TCACAGTGTGCTGCGCCATGCTTTTGAACCGCTATGAGGCTATGCTGACCCACTGCG 480
QY 532 CATGCCAAGTACTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
Db 481 CATGCCAAGTACTTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 592 GGGGCTGACATGATGAGCCCTTCTGCTTCAAGAGCTGCGCTTCTGCGCTGCG 651
Db 541 GGGGCTGACATGATGAGCCCTTCTGCTTCAAGAGCTGCGCTTCTGCGCTGCG 600
QY 652 AATATCTTTTCCATCTCTTACTGCTTACACCAAGATGTCATGAAGCTGGCTGATGAT 711
Db 601 AATATCTTTTCCATCTCTTACTGCTTACACCAAGATGTCATGAAGCTGGCTGATGAT 660
QY 712 ATCCGGGTCATATGCTGCTATGAGCTTATGCTATGCTATGCTATGCTATGCTATG 771
Db 661 ATCCGGGTCATATGCTGCTATGAGCTTATGCTATGCTATGCTATGCTATGCTATG 720
QY 772 CTTCATCTCTCTCTCATATCTGCTTATCTTAAAGCTGCTGCTGCTGCTGCTGCTG 831
Db 721 CTTCATCTCTCTCTCATATCTGCTTATCTTAAAGCTGCTGCTGCTGCTGCTGCTG 780
QY 832 GCCCAGGCGCAAGGATTTGGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
Db 781 GCCCAGGCGCAAGGATTTGGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 892 GTACCTTCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
Db 841 GTACCTTCATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 952 CCGCTCATCTTGGCGCAATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Db 901 CCGCTCATCTTGGCGCAATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
QY 1012 GGAAGTGAAGCAAGAGATTCGACAGCGCATCTTGAATTCATGCTGCTGCTGCTGCTG 1071
Db 961 GGAAGTGAAGCAAGAGATTCGACAGCGCATCTTGAATTCATGCTGCTGCTGCTGCTG 1020
QY 1072 GCTTCAGAGCCCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1131

Db 1021 GCTTCAGAGCCCTAGGTGATGATCAAACTTTTCATTAAGTCTCTGATTC 1080
 QY 1132 GATTATTAATGTTTACATTTTGAGAGACAGTATTCAGAAAAAATTTCTTAATAAAA 1191
 Db 1081 GATTATTAATGTTTACATTTTGAGAGACAGTATTCAGAAAAAATTTCTTAAT-AAAA 1139
 QY 1192 TACAAGTCGATGCTTCAATTAATGAAACGTGGGAAATCCCAATTTTTCATATTTAT 1251
 Db 1140 TACAAGTCGATGCTTCAATTAATGAAACGTGGGAAATCCCAATTTTTCATATTTAT 1199
 QY 1252 TTTCTTCTTGTGTTTCTGCTACATATAATTAATACCTGACTAGTTGTGGTTGCA 1311
 Db 1200 TTTCTTCTTGTGTTTCTGCTACATATAATTAATACCTGACTAGTTGTGGTTGCA 1259
 QY 1312 GGGTATTAATCTTTTCAATTTTACATGACGACGATCCCAATCTAAACT 1354
 Db 1260 GGGTATTAATCTTTTCAATTTTACATGACGACGATCCCAATCTAAACT 1302

RESULT 13

ACAS9982 standard; cDNA; 1302 BP.

ACAS9982:

10-JUN-2003 (first entry)

Prostate cancer therapy associated cDNA #663.

Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;

immunogen; cancer; prostate specific antigen; PSA;

prostatic acid phosphatase; PAP; prostate specific membrane antigen;

PSMA; gene; ss.

Homo sapiens.

US2002192763-A1.

19-DEC-2002.

29-JUN-2001; 2001US-0895793.

17-APR-2000; 2000US-157455P.

04-OCT-2000; 2000US-0679272.

28-MAR-2001; 2001US-0822827.

(XUJ/) XU J.

(DILL/) DILLON D C.

(MITC/) MITCHAM J L.

(HARL/) HARLOCKER S L.

(JIAN/) JIANG Y.

(KALO/) KALOS M D.

(FANG/) FANGER G R.

(RETT/) RETTER M W.

(STOL/) STOLK J A.

(DAYC/) DAY C H.

(VEDV/) VEDVICK T S.

(CART/) CARTER D.

(LISX/) LI S X.

(WANG/) WANG A.

(SKEI/) SKEIKY Y A W.

(HEPL/) HEPLER W T.

(HEND/) HENDERSON R A.

(HURA/) HURAL J.

(MCNE/) MCNETIL J D.

(HOUN/) HOUGHTON R L.

(DBAS/) Y DE BASSOLS C V.

(FOYT/) FOY T M.

XX MPI; 2003-352711/33.
 DR New fusion protein comprising prostate-specific polypeptides, or its
 PT immunogenic portions, useful for diagnosing, preventing and/or treating
 PT cancer, particularly prostate cancer
 XX Example 15; SEQ ID NO 916; 85pp; English.
 PS The invention describes a fusion protein comprising at least one amino
 CC acid sequence of immunogenic portions of any of the 3 sequences not
 CC defined in the specification, or sequences having at least 70 or 90 %
 CC sequence identity to any one of the 35 sequences defined in the USPTO
 CC web site, which is encoded by any of the 4 nucleotide sequences not
 CC defined in the specification. The fusion protein, composition and
 CC methods are useful for diagnosing, preventing and/or treating cancer,
 CC particularly prostate cancer. The proteins are useful as markers to
 CC indicate the presence or absence of cancer. This sequence
 CC represents a prostate cancer therapy associated cDNA.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from the US patent office at
 CC seqdata.uspto.gov/sequence.html?docID=US20020192763.

Sequence 1302 BP; 277 A; 346 C; 259 G; 420 T; 0 other;

Query Match 41.1%; Score 1287.8; DB 25; Length 1302;

Best Local Similarity 99.8%; Pred. No. 4.4e-257; Matches 1300; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 52 TGGACAAAGGGGGGTACACATTTCTTCATAGGGTTAGAGGCTTACCGCTGGGTGG 111
 Db 1 TGGACAAAGGGGGGTACACATTTCTTCATAGGGTTAGAGGCTTACCGCTGGGTGG 60
 QY 112 TCACAGTTCACTTTTCATAGTGTGTGATCCCAATGGAATGCAATGCTACATAC 171
 Db 61 TCACAGTTCACTTTTCATAGTGTGTGATCCCAATGGAATGCAATGCTACATAC 120
 QY 172 TTCATCTTAATAGGCTCCCTGTTTGAAGGCTCAGTCTGAGTGGCTTCCCATG 231
 Db 121 TTCATCTTAATAGGCTCCCTGTTTGAAGGCTCAGTCTGAGTGGCTTCCCATG 180
 QY 232 TGCCTCCTTACCTTATTTGCTGTGTGATGTAATGACAAATCTACATTTGCGGACT 291
 Db 181 TGCCTCCTTACCTTATTTGCTGTGTGATGTAATGACAAATCTACATTTGCGGACT 240
 QY 292 GAGCAAGCTGCGATGAGGCGCATGATATTTCTTTGCGATGCTTACAGCATGACATC 351
 Db 241 GAGCAAGCTGCGATGAGGCGCATGATATTTCTTTGCGATGCTTACAGCATGACATC 300
 QY 352 CTATCTCCACCTCATCCATGCGCCAAATGCTGGCATCTTCTGATCAATTCACATAC 411
 Db 301 CTATCTCCACCTCATCCATGCGCCAAATGCTGGCATCTTCTGATCAATTCACATAC 360
 QY 412 ATCCAGTTGATGCTGTGCTGTGATGATGATTTTGGCATGCTCCTTATGCGATGAA 471
 Db 361 ATCCAGTTGATGCTGTGCTGTGATGATGATTTTGGCATGCTCCTTATGCGATGAA 420
 QY 472 TCCACAGTGTCTGTGCGCATGAGCTTTTGAACCGCTATGTGCGCATCTGACCACTGCG 531
 Db 421 TCCACAGTGTCTGTGCGCATGAGCTTTTGAACCGCTATGTGCGCATCTGACCACTGCG 480
 QY 532 CATGCCAGTACTTACAGTGTGCTGTGATGCAACCAAAATGAGTGTGCGCTGTGCGG 591
 Db 481 CATGCCAGTACTTACAGTGTGCTGTGATGCAACCAAAATGAGTGTGCGCTGTGCGG 540
 QY 592 GGGGCTGCACTATGACACCCCTTCTGCTTCAATCAAGCAGCTGCTTGTGCGCTGC 651
 Db 541 GGGGCTGCACTATGACACCCCTTCTGCTTCAATCAAGCAGCTGCTTGTGCGCTGC 600
 QY 652 AATATCTTCCCATCTTACAGTGTGCTTACCAACCAAGTGCATGAAGCTGGCTGTGATAT 711
 Db 601 AATATCTTCCCATCTTACAGTGTGCTTACCAACCAAGTGCATGAAGCTGGCTGTGATAT 660


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QY 245 TATTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 304
DB 121 TATTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 180
QY 305 ATGAGGCCATGATATATTTCTTTGAGTCTTCAAGGATGACATCTCTCATCTCCACT 364
DB 181 ATGAGGCCATGATATATTTCTTTGAGTCTTCAAGGATGACATCTCTCATCTCCACT 240
QY 365 CATTCATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 424
DB 241 CATTCATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 300
QY 425 CTTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 484
DB 301 CTTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 360
QY 485 TGGCCATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 544
DB 361 TGGCCATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 420
QY 545 TTAAGTTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 604
DB 421 TTAAGTTCCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 480
QY 605 TGGCAACCTCTCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 664
DB 481 TGGCAACCTCTCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 540
QY 665 ATTCTCTAGTCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 724
DB 541 ATTCTCTAGTCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 600
QY 725 TGTCTATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 784
DB 601 TGTCTATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 660
QY 785 TCTCATATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 844
DB 661 TCTCATATGCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 720
QY 845 CATTTGGCACTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 904
DB 721 CATTTGGCACTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 780
QY 905 GATTGTCATGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 964
DB 781 GATTGTCATGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 840
QY 965 CCAATATCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 1024
DB 841 CCAATATCTGCTGCTAGTACTGACATCATCTACATTTGTGGGAGTGGAGCAGCCTGC 900
QY 1025 AGAAGTTTGGAGAGGCGCATCTTCCATTTTCCATGTTGGCCACACAGCCTTCAGAGCCTT 1084
DB 901 AGAAGTTTGGAGAGGCGCATCTTCCATTTTCCATGTTGGCCACACAGCCTTCAGAGCCTT 960
QY 1085 AGGTGTCA 1092
DB 961 AGGTGTCA 968

```

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KW anabolic; cytoskeletal; antiviral; gene therapy; cardiomyopathy; obesity;
KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
KW infection; human immunodeficiency virus; HIV; ds.
XX
OS Homo sapiens.
XX
XX WO200174904-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10241.
XX
XX 31-MAR-2000; 2000US-193664P.
XX 05-APR-2000; 2000US-194614P.
XX 06-APR-2000; 2000US-195063P.
XX 06-APR-2000; 2000US-195066P.
XX 06-APR-2000; 2000US-195067P.
XX 06-APR-2000; 2000US-195068P.
XX 06-APR-2000; 2000US-195069P.
XX 06-APR-2000; 2000US-195070P.
XX 06-APR-2000; 2000US-195510P.
XX 21-JUL-2000; 2000US-219855P.
XX 27-JUL-2000; 2000US-221284P.
XX 28-JUL-2000; 2000US-221325P.
XX 11-AUG-2000; 2000US-224588P.
XX 11-OCT-2000; 2000US-229613P.
XX 18-JAN-2001; 2001US-262508P.
XX 23-JAN-2001; 2001US-263433P.
XX 23-JAN-2001; 2001US-263604P.
XX 30-JAN-2001; 2001US-265161P.
XX 29-MAR-2001; 2001US-0823172.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Majumder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
XX Padigaru M, Mishra VS, Tchierne VT, Spytek KA, Li L;
XX Baumgartner JC, Gusev VY;
XX
XX WPI; 2001-639351/73.
XX
XX P-PSDB; ABA44534.
XX
XX New human G-protein coupled receptor X, GPCR, polypeptide useful in
XX treatment or prevention of GPCR associated disorders e.g.
XX cardiomyopathy or atherosclerosis, and to screen for antagonists and
XX agonists useful therapeutically.
XX
XX Claim 9; Page 57; 157pp; English.
XX
XX The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
XX encode G-coupled protein-receptor related polypeptides
XX (ABA44523-ABA44543). The isolated polypeptide having a sequence differing
XX by no more than 15 % of amino acid residues from one of 22 amino acid
XX sequences (or mature forms of the sequences), fully defined in the
XX specification and corresponding to human G-protein coupled receptor X
XX (GPCR) polypeptides. The polypeptides have potential cardiant,
XX antiarteriosclerotic, anabolic, cytoskeletal and antiviral activity. The
XX polypeptides can be administered therapeutically, especially using gene
XX therapy and expressing the encoding DNA in vivo, to treat or prevent
XX GPCR-associated disorders, especially in humans. For example, they can
XX be used to treat/prevent cardiomyopathy, atherosclerosis, disorders
XX related to signal processing and metabolic pathway modulation (e.g.
XX obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
XX sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
XX disease, Parkinson's disorder, Huntington's disease), immune disorders,
XX haematopoietic disorders, developmental diseases, neurological disorders,
XX bacterial, fungal, protozoal and viral infections (e.g. with human
XX immunodeficiency virus (HIV-1 or HIV-2)). They can be used diagnostically
XX to determine the presence of or predisposition to a disease associated
XX with altered levels of the polypeptide in mammals (especially humans) by
XX detecting alterations in polypeptide expression levels relative to
XX control samples. They are useful to identify agents binding polypeptide
XX (e.g. cellular receptors or downstream effectors) and/or agents

```


Db 244 IGVLAFFVYVPLIGLSVYHFRGNSLHPYIVRVVMDIYLLPVPINPIYGAKTQIRTRVLA 303
Qy 306 RLFFVA 311
Db 304 AMFKIS 309

RESULT 2
US-08-465-980-2
Sequence 2, Application US/08465980
Patent No. 5756309
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-980-2

Query Match 59.6%; Score 964.5; DB 1; Length 320;
Best Local Similarity 59.4%; Pred. No. 2.6e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;
Qy 15 ILGLGLEBAQWLAFLPCLSLYLAVLGNLTIIYVTRTSHLHEBMYFLCMLSGDIL 74
Db 12 VLIIGLEBAHFWGFPPLSMYVVMCGNCIVFVTRTSHLAPMYFLCMLAIDLA 71
Qy 75 ISTDSPKMLAIFWPNSTTIQPDACLLQIFAHSLSGMESTVLLMAFPDYVAICPLRH 134
Db 72 LSTSTPKLIALFWPDSREISERACTQMFPIHALSAISTILLMAFPDYVAICPLRH 131
Qy 135 ATVLTLPRTYKIGVAAVVRGALMAPLPVFYKQLPFCRSNITLSHSYCLHODVWKLACDDI 194
Db 132 AAVLNTVTVAQIGIVAVRGSLEFFPLPIIKRLAFCHSNVLSHSYCVHODVWKLAVADT 191
Qy 195 RVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAQAKAFGCVSHVCAVFIY 253
Db 192 LRVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAQAKAFGCVSHVCAVFIY 251
Qy 254 VPIGLSMVHRFSKRSDPLPVILANTYLLVPPVNLPIYGVTKYKIRIIRLFFVA 311
Db 252 VPIGLSVVHRFNSLHPYIVRVVMDIYLLPVPINPIYGAKTQIRTRVLA 309

Db 252 VPIGLSVVHRFNSLHPYIVRVVMDIYLLPVPINPIYGAKTQIRTRVLA 309
RESULT 3
US-09-053-303-2
Sequence 2, Application US/09053303
Patent No. 5948890
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRJ70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,303
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-053-303-2

Query Match 59.6%; Score 964.5; DB 2; Length 320;
Best Local Similarity 59.4%; Pred. No. 2.6e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;
Qy 15 ILGLGLEBAQWLAFLPCLSLYLAVLGNLTIIYVTRTSHLHEBMYFLCMLSGDIL 74
Db 12 VLIIGLEBAHFWGFPPLSMYVVMCGNCIVFVTRTSHLAPMYFLCMLAIDLA 71
Qy 75 ISTDSPKMLAIFWPNSTTIQPDACLLQIFAHSLSGMESTVLLMAFPDYVAICPLRH 134
Db 72 LSTSTPKLIALFWPDSREISERACTQMFPIHALSAISTILLMAFPDYVAICPLRH 131
Qy 135 ATVLTLPRTYKIGVAAVVRGALMAPLPVFYKQLPFCRSNITLSHSYCLHODVWKLACDDI 194
Db 132 AAVLNTVTVAQIGIVAVRGSLEFFPLPIIKRLAFCHSNVLSHSYCVHODVWKLAVADT 191
Qy 195 RVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAQAKAFGCVSHVCAVFIY 253
Db 192 LRVNVVGLIYVISAIGDLSLISFSYLLIKTVLGL-TREAQAKAFGCVSHVCAVFIY 251
Qy 254 VPIGLSMVHRFSKRSDPLPVILANTYLLVPPVNLPIYGVTKYKIRIIRLFFVA 311
Db 252 VPIGLSVVHRFNSLHPYIVRVVMDIYLLPVPINPIYGAKTQIRTRVLA 309

RESULT 4
US-09-339-115-2
Sequence 2, Application US/0939115
Patent No. 6372891
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-339-115-2

Query Match 59.6%; Score 964.5; DB 4; Length 320;
Best Local Similarity 59.4%; Pred. No. 2.6e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;
QY 15 ILIGPGLAEQFWLAFPLCSLYLAVGNLTIIYVTEHSLHEPMYFLCMLSGIDIL 74
DB 12 VLIIGPGLAEQFWLAFPLCSLYLAVGNLTIIYVTEHSLHEPMYFLCMLSGIDIL 71
QY 75 ISTSSMPKMLAIFWENSTTIQFDACILQIFAIHSISGNESTVLLAMAFDRYVAICHPLRH 134
DB 72 LSTSTMPKMLAIFWENSTTIQFDACILQIFAIHSISGNESTVLLAMAFDRYVAICHPLRH 131
QY 135 ATVLTLPRTYKIGVAAVVGALMAPLPVFIRKQLPFCRSNLTSHSYCVHODVMKLAADDI 194
DB 132 AAVLNTTAAQIGIAVAVRGSLEFPPLPLIKRLAFCHSNVLSHSYCVHODVMKLAADT 191
QY 195 RVNVVYGLIIVISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVFIY 253
DB 192 LRVNVYGLIIVISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVFIY 251
QY 254 VPFILGSMVHRGSKRDSPLPYILANTYLLVPPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 311
DB 252 VPLIGLSVVRHFGNSLHPIVRVVMGDIYLLPVPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 309

RESULT 5

PCT-US95-07093-2
Sequence 2, Application PC/TUS9507093
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07093-2

Query Match 59.6%; Score 964.5; DB 5; Length 320;
Best Local Similarity 59.4%; Pred. No. 2.6e-80;
Matches 177; Conservative 54; Mismatches 66; Indels 1; Gaps 1;
QY 15 ILIGPGLAEQFWLAFPLCSLYLAVGNLTIIYVTEHSLHEPMYFLCMLSGIDIL 74
DB 12 VLIIGPGLAEQFWLAFPLCSLYLAVGNLTIIYVTEHSLHEPMYFLCMLSGIDIL 71
QY 75 ISTSSMPKMLAIFWENSTTIQFDACILQIFAIHSISGNESTVLLAMAFDRYVAICHPLRH 134
DB 72 LSTSTMPKMLAIFWENSTTIQFDACILQIFAIHSISGNESTVLLAMAFDRYVAICHPLRH 131
QY 135 ATVLTLPRTYKIGVAAVVGALMAPLPVFIRKQLPFCRSNLTSHSYCVHODVMKLAADDI 194
DB 132 AAVLNTTAAQIGIAVAVRGSLEFPPLPLIKRLAFCHSNVLSHSYCVHODVMKLAADT 191
QY 195 RVNVVYGLIIVISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVFIY 253
DB 192 LRVNVYGLIIVISAIGLDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVCAVFIY 251
QY 254 VPFILGSMVHRGSKRDSPLPYILANTYLLVPPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 311
DB 252 VPLIGLSVVRHFGNSLHPIVRVVMGDIYLLPVPVLPVLPVLPVLPVLPVLPVLPVLPVLPV 309

RESULT 6
US-08-988-876-7
Sequence 7, Application US/08988876
Patent No. 6063596

```

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988, 876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 32086
US-08-988-876-7

Query Match 26.4%; Score 427.5; DB 3; Length 314;
Best Local Similarity 34.5%; Pred. No. 2.2e-31;
Matches 108; Conservative 64; Mismatches 120; Indels 21; Gaps 8;

```

```

RESULT 7
US-08-988-876-5
Sequence 5, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988, 876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1314667
US-08-988-876-5

Query Match 24.4%; Score 394.5; DB 3; Length 309;
Best Local Similarity 29.0%; Pred. No. 2.1e-28;
Matches 87; Conservative 76; Mismatches 126; Indels 11; Gaps 5;

```


Db 243 SHLSVSLRYCTSLGVYSSAAPSHTSS-----VASVYTVVTPMLPFITSLNKKDK 298

RESULT 8
US-08-988-876-6

Sequence 6, Application US/08988876
Patent No. 6063596

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED

TITLE OF INVENTION: WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 333 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 205814

US-08-988-876-6

Query Match

Best Local Similarity 23.7%; Score 383; DB 3; Length 333;

Matches 94; Conservative 73; Mismatches 133; Indels 32; Gaps 9;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Qy 238 AFGTCVSHCAVFIFVYVPIGLSMVHFRSKRDSPLVILANI-YLLVPEVLPNIYGVK 296

Db 237 AFGTCVSHCAVFIFVYVPIGLSMVHFRSKRDSPLVILANI-YLLVPEVLPNIYGVK 293

Qy 297 TKRIRQ-----RILRLFHVATH 313

Db 294 NKDVSVLKKTLCEBYIRSPPSILHFLVLCR 325

RESULT 9
US-09-465-901-48

Sequence 48, Application US/09465901
Patent No. 6492143

GENERAL INFORMATION:

APPLICANT: Reed, Randall

APPLICANT: Kautzurst, Dietmar

TITLE OF INVENTION: Olfactory Receptor Expression Libraries

TITLE OF INVENTION: ad Methods of Making and Using Them

FILE REFERENCE: 00107.00105

CURRENT APPLICATION NUMBER: US/09/465,901

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: 60/112,605

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 48

LENGTH: 313

TYPE: PRT

ORGANISM: Mus musculus

FEATURE:

OTHER INFORMATION: PCR primer

US-09-465-901-48

Query Match

Best Local Similarity 23.1%; Score 374; DB 4; Length 313;

Matches 98; Conservative 56; Mismatches 137; Indels 10; Gaps 6;

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 OPERATING SYSTEM: IBM PC COMPATIBLE
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 296 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-948A-2

Query Match 22.7%; Score 367; DB 2; Length 296;
 Best Local Similarity 32.2%; Pred. No. 6.5e-26;
 Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;
 QY 7 NESAATYFLLGL---PGLBAQFWLAFPLCSL-YLIAVGNLTIIYVTEHSLHEPMY 62
 DB 8 NQWVTEFLGLGFLGRIO---MLFGLPSLFYVFTLLGNGTLLGLSLDSRLHTPMY 63
 QY 63 IFCLMSGIDILISTSSMPKMLAFWNSSTTIOFDACLOIFAIHSLSGNESTVLLAMAF 122
 DB 64 FFLSHLAVNVAACNTVPQMLVNLHPAKPISFAGCMTDLPFLSPAHTECLLVLMYSY 123
 QY 123 DRYVAICHPLRHAIVTLPLRVTKIGVAAVRGAAALMAPLVFIKQDPFGRSNILSHSYCL 182
 DB 124 DRYVAICHPLRHAIVTLPLRVTKIGVAAVRGAAALMAPLVFIKQDPFGRSNILSHSYCL 183
 QY 183 HQDWKLAACDDIRVN--VYVGLVVIISAGLSDLLISFSYLL--ILKTVGLTREAOAKA 238
 DB 184 ILTVRLACADVTMNOVVFECMFLVGPLCLVLSYSHILGILRIQSG--EGRRKA 240
 QY 239 FGLTGVSHCAVFIYVFFIGLSWVHRFSKRRDSPFLPILANITYLVPPVLP 290
 DB 241 FSTCSSLICVVGFLFSGAIVYMAPK-SRHPBQOKVLLILOFLSTPMK 291

RESULT 11
 US-08-467-947A-2
 ; Sequence 2, Application US/08467947A
 ; Patent No. 6090575
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; APPLICANT: CAO, LIANG
 ; APPLICANT: NI, JIAN

APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 OPERATING SYSTEM: IBM PC COMPATIBLE
 SOFTWARE: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 296 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-947A-2

Query Match 22.7%; Score 367; DB 3; Length 296;
 Best Local Similarity 32.2%; Pred. No. 6.5e-26;
 Matches 94; Conservative 61; Mismatches 121; Indels 16; Gaps 7;
 QY 7 NESAATYFLLGL---PGLBAQFWLAFPLCSL-YLIAVGNLTIIYVTEHSLHEPMY 62
 DB 8 NQWVTEFLGLGFLGRIO---MLFGLPSLFYVFTLLGNGTLLGLSLDSRLHTPMY 63
 QY 63 IFCLMSGIDILISTSSMPKMLAFWNSSTTIOFDACLOIFAIHSLSGNESTVLLAMAF 122
 DB 64 FFLSHLAVNVAACNTVPQMLVNLHPAKPISFAGCMTDLPFLSPAHTECLLVLMYSY 123
 QY 123 DRYVAICHPLRHAIVTLPLRVTKIGVAAVRGAAALMAPLVFIKQDPFGRSNILSHSYCL 182
 DB 124 DRYVAICHPLRHAIVTLPLRVTKIGVAAVRGAAALMAPLVFIKQDPFGRSNILSHSYCL 183
 QY 183 HQDWKLAACDDIRVN--VYVGLVVIISAGLSDLLISFSYLL--ILKTVGLTREAOAKA 238
 DB 184 ILTVRLACADVTMNOVVFECMFLVGPLCLVLSYSHILGILRIQSG--EGRRKA 240
 QY 239 FGLTGVSHCAVFIYVFFIGLSWVHRFSKRRDSPFLPILANITYLVPPVLP 290
 DB 241 FSTCSSLICVVGFLFSGAIVYMAPK-SRHPBQOKVLLILOFLSTPMK 291

RESULT 12
 US-08-465-980-3
 ; Sequence 3, Application US/08465980
 ; Patent No. 5756309
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel R.
 ; APPLICANT: LI, YI

APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-980-3

Query Match 22.1%; Score 357.5; DB 1; Length 247;
Best Local Similarity 36.5%; Pred. No. 3,9e-25;
Matches 93; Conservative 46; Mismatches 99; Indels 17; Gaps 6;

QY 14 FILIGPGLBEAOFMLAPFLCSLYLAVNGNTIIVYVTHSHPEMYIFLCMSGDI 73
DB 1 FILIGPPOPEQONLCYALFLAMVLTLLGNLLIIVLRDSDHLPMTFLSNLSFSDL 60
QY 74 LISTSMPTALIFWNSSTTIOFDACLIQIFAIHSLGMSSTVLLAMADRYVAICPLR 133
DB 61 CFSSTVITPRLQNMQNDPSIPYADCTQMYFLLFGDLSEFLVAMAYDRVAICFPL- 119
QY 134 HATVLTLPVYTKIGA--AVVRGAALMAPLVPFIKQLPFCRSNLSHSYCLHODVMKLA 190
DB 120 HTTAISMPLCLALVALSWLTTFFAMLHTL--LVARLCFCADNVIPHFCDMSALLKLA 177
QY 191 CDDIRVN-----VYGLIIVISAGDSLLISFSYLLIKTVLGL-TREAQAKAFGTGVS 244
DB 178 FSDTRNEMVITFIMGGLIIVT-----PFLILGSYARIYSSILAVPSKGIKAFSTGCS 232
QY 245 HVCANFIYVPIGL 259
DB 233 HLSVSLFYGTIVGL 247

RESULT 13

US-09-053-303-3
Sequence 3, Application US/09053303
Patent No. 5948890
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,303
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-053-303-3

Query Match 22.1%; Score 357.5; DB 2; Length 247;
Best Local Similarity 36.5%; Pred. No. 3,9e-25;
Matches 93; Conservative 46; Mismatches 99; Indels 17; Gaps 6;

QY 14 FILIGPGLBEAOFMLAPFLCSLYLAVNGNTIIVYVTHSHPEMYIFLCMSGDI 73
DB 1 FILIGPPOPEQONLCYALFLAMVLTLLGNLLIIVLRDSDHLPMTFLSNLSFSDL 60
QY 74 LISTSMPTALIFWNSSTTIOFDACLIQIFAIHSLGMSSTVLLAMADRYVAICPLR 133
DB 61 CFSSTVITPRLQNMQNDPSIPYADCTQMYFLLFGDLSEFLVAMAYDRVAICFPL- 119
QY 134 HATVLTLPVYTKIGA--AVVRGAALMAPLVPFIKQLPFCRSNLSHSYCLHODVMKLA 190
DB 120 HTTAISMPLCLALVALSWLTTFFAMLHTL--LVARLCFCADNVIPHFCDMSALLKLA 177
QY 191 CDDIRVN-----VYGLIIVISAGDSLLISFSYLLIKTVLGL-TREAQAKAFGTGVS 244
DB 178 FSDTRNEMVITFIMGGLIIVT-----PFLILGSYARIYSSILAVPSKGIKAFSTGCS 232
QY 245 HVCANFIYVPIGL 259
DB 233 HLSVSLFYGTIVGL 247

RESULT 14

US-09-339-115-3
Sequence 3, Application US/09339115
Patent No. 6372891
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
CORRESPONDENCE ADDRESS:

Tue Feb 10 06:04:26 2004

us-10-017-066a-2.ral

Page 8

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESS: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-339-115-3

Query Match 22.1%; Score 357.5; DB 4; Length 247;
Best Local Similarity 36.5%; Pred. No. 3.9e-25;
Matches 93; Conservative 46; Mismatches 99; Indels 17; Gaps 6;
QY 14 FILIGLPLEEACQFWLAFPLCSYLIVLAVGNLTIIYIVRTEHSLHEPMYIFLCYLSGIDI 73
DB 1 FLLGLPIQPEQQLCYALFLAWLITLGNLIIIVIRDSHLHTMPLFLSNLSFSDL 60
QY 74 LISTSSMPKMLAFWENSTTIQPDACLLQIFAIHSLSGMSSTVLLAMAFDRYVAICHPLR 133
DB 61 CFSSVTIPKLLQNNQNDPSIPYADCLTQWYFLLFGDLESFLVAMAYDRYVAICFPL- 119
QY 134 HATVLTLPRTKIGVA--AVVRGALMAPLPVFIKQLPFCRSNIISHSYCLHODWKLA 190
DB 120 HTYHNSPMLCALVALSWLITTFHAMLHTL--LMARLCFCADNVLPFPCDMSALIKLA 177
QY 191 CDDIRN----VYGLIVITSAIGLDSLLISFSYLLIKTVGL-TREAQARAGTCVS 244
DB 178 FSDTRVNEWVIFMGHILVI-----PFLILGSYARIVSILKVPSSKICAFSTGCS 232
QY 245 HVCAPFFIYVPFGL 259
DB 233 HLSVSLFYGTIVGL 247

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1744
TELEFAX: 201-994-1700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07093-3

Query Match 22.1%; Score 357.5; DB 5; Length 247;
Best Local Similarity 36.5%; Pred. No. 3.9e-25;
Matches 93; Conservative 46; Mismatches 99; Indels 17; Gaps 6;
QY 14 FILIGLPLEEACQFWLAFPLCSYLIVLAVGNLTIIYIVRTEHSLHEPMYIFLCYLSGIDI 73
DB 1 FLLGLPIQPEQQLCYALFLAWLITLGNLIIIVIRDSHLHTMPLFLSNLSFSDL 60
QY 74 LISTSSMPKMLAFWENSTTIQPDACLLQIFAIHSLSGMSSTVLLAMAFDRYVAICHPLR 133
DB 61 CFSSVTIPKLLQNNQNDPSIPYADCLTQWYFLLFGDLESFLVAMAYDRYVAICFPL- 119
QY 134 HATVLTLPRTKIGVA--AVVRGALMAPLPVFIKQLPFCRSNIISHSYCLHODWKLA 190
DB 120 HTYHNSPMLCALVALSWLITTFHAMLHTL--LMARLCFCADNVLPFPCDMSALIKLA 177
QY 191 CDDIRN----VYGLIVITSAIGLDSLLISFSYLLIKTVGL-TREAQARAGTCVS 244
DB 178 FSDTRVNEWVIFMGHILVI-----PFLILGSYARIVSILKVPSSKICAFSTGCS 232
QY 245 HVCAPFFIYVPFGL 259
DB 233 HLSVSLFYGTIVGL 247

Search completed: February 9, 2004, 16:26:17
Job time : 22 sec

Tue Feb 10 06:04:27 2004

us-10-017-066a-2.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 16:25:17 ; Search time 33 Seconds

(without alignments)
2011.339 Million cell updates/sec

Title: US-10-017-066A-2
Perfect score: 1617
Sequence: 1 MVDPNGNSATYFILGLP.....KEIRORILFLHVATASRP 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PC7US_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1617	100.0	317	15	US-10-205-823-443 Sequence 443, App
2	1617	100.0	318	15	US-10-001-469-2880 Sequence 2880, App
3	1617	99.8	317	12	US-10-295-027-873 Sequence 873, App
4	1614	99.8	317	12	US-10-293-798-746 Sequence 746, App
5	1614	99.8	318	9	US-09-759-143-920 Sequence 920, App
6	1614	99.8	318	9	US-09-780-669-920 Sequence 920, App
7	1614	99.8	318	9	US-09-822-827-920 Sequence 920, App
8	1614	99.8	318	10	US-09-886-055-91 Sequence 91, App1
9	1614	99.8	318	10	US-09-895-793-920 Sequence 920, App
10	1614	99.8	318	10	US-09-895-814-920 Sequence 920, App
11	1614	99.8	318	11	US-09-966-459A-2 Sequence 2, App1
12	1614	99.8	318	11	US-09-804-291-91 Sequence 91, App1
13	1614	99.8	318	12	US-10-017-161-868 Sequence 868, App
14	1614	99.8	318	12	US-10-144-678A-920 Sequence 920, App
15	1614	99.8	318	12	US-10-294-025-920 Sequence 920, App

16	1614	99.8	318	12	US-10-044-643-26	Sequence 26, App1
17	1614	99.8	318	14	US-10-012-896-920	Sequence 920, App
18	1614	99.8	318	15	US-10-225-567A-434	Sequence 434, App
19	1607	99.4	318	12	US-10-044-643-28	Sequence 28, App1
20	1607	99.4	318	12	US-10-044-643-30	Sequence 30, App1
21	1542	95.4	303	15	US-10-001-469-2887	Sequence 2887, App
22	1534	94.9	302	15	US-10-001-469-2882	Sequence 2882, App
23	1515	93.7	298	15	US-10-001-469-2883	Sequence 2883, App
24	1515	93.7	298	15	US-10-001-469-2885	Sequence 2885, App
25	1262	78.0	249	12	US-10-114-669-8894	Sequence 8894, App
26	985	60.9	320	12	US-10-005-041A-42	Sequence 42, App1
27	979	60.5	318	15	US-10-024-399-18	Sequence 18, App1
28	979	60.5	320	9	US-09-759-143-527	Sequence 527, App1
29	979	60.5	320	9	US-09-730-018-7	Sequence 7, App1
30	979	60.5	320	9	US-09-780-669-527	Sequence 527, App1
31	979	60.5	320	9	US-09-822-827-527	Sequence 527, App1
32	979	60.5	320	10	US-09-886-055-83	Sequence 83, App1
33	979	60.5	320	10	US-09-868-033C-4	Sequence 4, App1
34	979	60.5	320	10	US-09-895-793-527	Sequence 527, App
35	979	60.5	320	10	US-09-895-814-527	Sequence 527, App
36	979	60.5	320	11	US-09-804-291-83	Sequence 83, App1
37	979	60.5	320	12	US-10-144-678A-527	Sequence 527, App
38	979	60.5	320	12	US-10-294-025-527	Sequence 527, App
39	979	60.5	320	12	US-10-044-643-65	Sequence 65, App1
40	979	60.5	320	12	US-10-431-842-7	Sequence 7, App1
41	979	60.5	320	12	US-10-025-806-34	Sequence 34, App1
42	979	60.5	320	12	US-10-387-629-200	Sequence 200, App
43	979	60.5	320	12	US-10-005-041A-41	Sequence 41, App1
44	979	60.5	320	12	US-09-581-566A-55	Sequence 55, App1
45	979	60.5	320	14	US-10-012-896-527	Sequence 527, App

ALIGNMENTS

RESULT 1
US-10-205-823-443
Sequence 443, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kanakatti, Shubhangi
APPLICANT: Monsey, Angela W.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 443
LENGTH: 317
TYPE: PRT
ORGANISM: Homo sapiens

US-10-205-823-443

Query Match 100.0%; Score 1617; DB 15; Length 317;
Best Local Similarity 100.0%; Pred. No. 5,9e-150;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVDNNGNSATYFLLGLPGLBQAQWLAFLPLCSLYLAVLGNLTIIYVREHSLSHP 60
DB 1 WVDNNGNSATYFLLGLPGLBQAQWLAFLPLCSLYLAVLGNLTIIYVREHSLSHP 60
QY MYFLCMLSGDILISTSSMPKMLAIFWNSSTTIOFDACLIQIPAHLSGMSSTVLLAM 120
DB MYFLCMLSGDILISTSSMPKMLAIFWNSSTTIOFDACLIQIPAHLSGMSSTVLLAM 120
QY 121 AFDRYVAICHPLRHATVTLTPRVTKIGVAAVVGALMAPLPVFIKQLPFCRSNLSHSY 180
DB 121 AFDRYVAICHPLRHATVTLTPRVTKIGVAAVVGALMAPLPVFIKQLPFCRSNLSHSY 180
QY 181 CHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSLILKTVLGLTREAOAKAFG 240
DB 181 CHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSLILKTVLGLTREAOAKAFG 240
QY 241 TCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYILANLYLVPPVLPNIYGVYKKEI 300
DB 241 TCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYILANLYLVPPVLPNIYGVYKKEI 300
QY 301 RORILRLPHVATHASEP 317
DB 301 RORILRLPHVATHASEP 317

RESULT 2
US-10-001-469-2880Sequence 2880, Application US/10001469
Publication No. US20030091562A1

GENERAL INFORMATION:
APPLICANT: JAKOBOWITS, AVA
APPLICANT: RAYTANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: SAFERAN, DOUGLAS
APPLICANT: HUBERT, RENE
APPLICANT: PARIS, MARY
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
FILE REFERENCE: 51158-20024.20
CURRENT APPLICATION NUMBER: US/10/001,469
PRIOR FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/157,902
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/291,118
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 09/680,728
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 2888
SOFTWARE: patentin Ver. 2.1
SEQ ID NO 2880
LENGTH: 318
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: 10133A11 encoded amino
US-10-001-469-2880

Query Match 100.0%; Score 1617; DB 15; Length 318;
Best Local Similarity 100.0%; Pred. No. 5,9e-150;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVDNNGNSATYFLLGLPGLBQAQWLAFLPLCSLYLAVLGNLTIIYVREHSLSHP 60
DB 2 WVDNNGNSATYFLLGLPGLBQAQWLAFLPLCSLYLAVLGNLTIIYVREHSLSHP 61

QY 61 MYFLCMLSGDILISTSSMPKMLAIFWNSSTTIOFDACLIQIPAHLSGMSSTVLLAM 120
DB 62 MYFLCMLSGDILISTSSMPKMLAIFWNSSTTIOFDACLIQIPAHLSGMSSTVLLAM 121
QY 121 AFDRYVAICHPLRHATVTLTPRVTKIGVAAVVGALMAPLPVFIKQLPFCRSNLSHSY 180
DB 122 AFDRYVAICHPLRHATVTLTPRVTKIGVAAVVGALMAPLPVFIKQLPFCRSNLSHSY 181
QY 181 CHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSLILKTVLGLTREAOAKAFG 240
DB 182 CHQDVMLACDDIRVNVVYGLIVISAIGDSLISFSLILKTVLGLTREAOAKAFG 241
QY 241 TCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYILANLYLVPPVLPNIYGVYKKEI 300
DB 242 TCVSHVCAVFIFYVPFISLWHRFSKRDSPLPYILANLYLVPPVLPNIYGVYKKEI 301
QY 301 RORILRLPHVATHASEP 317
DB 302 RORILRLPHVATHASEP 318

RESULT 3

US-10-295-027-873

Sequence 873, Application US/10295027
Publication No. US2003023250A1

GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevez, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
TITLE OF INVENTION: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: patentin Ver. 2.1
SEQ ID NO 873
LENGTH: 317
TYPE: PRT
ORGANISM: Homo sapiens

US-10-295-027-873

Query Match 99.8%; Score 1614; DB 12; Length 317;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPNGNESSATYFIIIGLPGLEAOFWLAFLCSYLAVGNLTIIYVREHSLHEP 60
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 QY 61 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 120
 DB 61 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 120
 QY 121 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 180
 DB 121 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 180
 QY 181 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
 DB 181 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
 QY 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300
 DB 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300
 QY 301 RORILRLFHVATHASEP 317
 DB 301 RORILRLFHVATHASEP 317

RESULT 4

US-10-292-798-746
 ; Sequence 746, Application US/10292798
 ; Publication No. US2003023583A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: ABURATANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRI-PHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2070
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 746
 ; LENGTH: 317
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-292-798-746

Query Match 99.8%; Score 1614; DB 12; Length 317;
 Best Local Similarity 99.7%; Pred. No. 1.2e-149;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPNGNESSATYFIIIGLPGLEAOFWLAFLCSYLAVGNLTIIYVREHSLHEP 60
 DB 1 MDPNGNESSATYFIIIGLPGLEAOFWLAFLCSYLAVGNLTIIYVREHSLHEP 60
 QY 61 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 120
 DB 61 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 120
 QY 121 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 180
 DB 121 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 180
 QY 181 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
 DB 181 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
 QY 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300
 DB 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300

DB 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300
 QY 301 RORILRLFHVATHASEP 317
 DB 301 RORILRLFHVATHASEP 317

RESULT 5

US-09-759-143-920
 ; Sequence 920, Application US/09759143
 ; Patent No. US20020022248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiaqichun
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiaq, Yugu
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darriek
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE REFERENCE: 210121.427023
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: PaateSeq for Windows Version 3.0
 ; SEQ ID NO 920
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-759-143-920

Query Match 99.8%; Score 1614; DB 9; Length 318;
 Best Local Similarity 99.7%; Pred. No. 1.2e-149;
 Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPNGNESSATYFIIIGLPGLEAOFWLAFLCSYLAVGNLTIIYVREHSLHEP 60
 DB 2 MDPNGNESSATYFIIIGLPGLEAOFWLAFLCSYLAVGNLTIIYVREHSLHEP 61
 QY 61 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 120
 DB 62 MYIFLCMLSGIDILLISTSSMPKMLAFWENSTTIQDACLIOFAIHSISGMESTVLLAM 121
 QY 121 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 180
 DB 122 AFRYVAICHPLEHATVLTLPRTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIIISHSY 181
 QY 181 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
 DB 182 CHQDVMKACDDIRVNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
 QY 241 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 300
 DB 242 TCVSHCAVFIFFVPIFGLSMWRFSKRDSPPLVILANIYLLVPPVLPPIYGVKTKKEI 301
 QY 301 RORILRLFHVATHASEP 317
 DB 302 RORILRLFHVATHASEP 318

RESULT 6
 US-09-780-669-920

Sequence 920, Application us/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-780-669-920

Query Match 99.8%; Score 1614; DB 9; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 60
2 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 61
QY MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 120
Db 62 MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 121
QY 121 AFDRYVAICHPRLRAATVTLPRVTKIGVAAVVGALMAPLPVFIKOLPFCRSNLSHSY 180
Db 122 AFDRYVAICHPRLRAATVTLPRVTKIGVAAVVGALMAPLPVFIKOLPFCRSNLSHSY 181
QY 181 CHODVWKLACDDIRAVVYVGLIYIISAGIDSLISFVLLIKTVGLTREDAQAFG 240
Db 182 CHODVWKLACDDIRAVVYVGLIYIISAGIDSLISFVLLIKTVGLTREDAQAFG 241
QY 241 TCVSHVCAVFIYVFPFGLSMVHRFSKRDSPLFVILANTYLLVPVLPNIYGVKTKEI 300
Db 242 TCVSHVCAVFIYVFPFGLSMVHRFSKRDSPLFVILANTYLLVPVLPNIYGVKTKEI 301
QY 301 RORILRLFHVATHASEP 317
Db 302 RORILRLFHVATHASEP 318

RESULT 7
US-09-822-827-920
Sequence 920, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822.827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-822-827-920

Query Match 99.8%; Score 1614; DB 9; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 60
2 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 61
QY MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 120
Db 62 MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 121
QY 121 AFDRYVAICHPRLRAATVTLPRVTKIGVAAVVGALMAPLPVFIKOLPFCRSNLSHSY 180
Db 122 AFDRYVAICHPRLRAATVTLPRVTKIGVAAVVGALMAPLPVFIKOLPFCRSNLSHSY 181
QY 181 CHODVWKLACDDIRAVVYVGLIYIISAGIDSLISFVLLIKTVGLTREDAQAFG 240
Db 182 CHODVWKLACDDIRAVVYVGLIYIISAGIDSLISFVLLIKTVGLTREDAQAFG 241
QY 241 TCVSHVCAVFIYVFPFGLSMVHRFSKRDSPLFVILANTYLLVPVLPNIYGVKTKEI 300
Db 242 TCVSHVCAVFIYVFPFGLSMVHRFSKRDSPLFVILANTYLLVPVLPNIYGVKTKEI 301
QY 301 RORILRLFHVATHASEP 317
Db 302 RORILRLFHVATHASEP 318

RESULT 8
US-09-886-055-91
Sequence 91, Application US/09886055
Patent No. US20020132273A1
GENERAL INFORMATION:
APPLICANT: STREY, LOBERT
APPLICANT: ZOZULYA, SERGEY
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
FILE REFERENCE: 078003-0277150
CURRENT APPLICATION NUMBER: US/09/886.055
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,812
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 91
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-055-91

Query Match 99.8%; Score 1614; DB 10; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 60
2 MWDPNNGESSATYFILGLPGLBEOQFWLAFPLCSLYLAIVGNLTIIYIVRTHSLHEP 61
QY MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 120
Db 62 MYFLCMLSGIDILISTSSMPKMLAFWPNSTTIQDACLQIFAIHSLSGMESTVLLAM 121

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QY 121 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 180
DB 122 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 181
QY 181 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
DB 182 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
QY 241 TCVSHVCAVFIFFYPFICLSWVHRSKRSDPLPVIIANIIYLVPEVLPNPIYGVYKTKEI 300
DB 242 TCVSHVCAVFIFFYPFICLSWVHRSKRSDPLPVIIANIIYLVPEVLPNPIYGVYKTKEI 301
QY 301 RORIRLRFHVATHASEP 317
DB 302 RORIRLRFHVATHASEP 318
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RESULT 9

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US-09-895-793-920
; Sequence 920, Application US/09895793
; Publication No. US20020192763A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-895-793-920
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Query Match 99.8%; Score 1614; DB 10; Length 318;
Best Local Similarity 99.7%; Pred. No. 1,2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPNGNSESATYFIIIGLPGLEAOFWLAFLCSYLVANIGNTIIYVTRTHSHLP 60
DB 2 MDPNGNSESATYFIIIGLPGLEAOFWLAFLCSYLVANIGNTIIYVTRTHSHLP 61
QY 61 MYIFCLMSGIDILISTSSMPKMLAIFWNSSTIIQFDACILQMFALHSLSGNESTVLLAM 120
DB 62 MYIFCLMSGIDILISTSSMPKMLAIFWNSSTIIQFDACILQMFALHSLSGNESTVLLAM 121
QY 121 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 180
DB 122 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 181
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QY 181 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
DB 182 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
QY 241 TCVSHVCAVFIFFYPFICLSWVHRSKRSDPLPVIIANIIYLVPEVLPNPIYGVYKTKEI 300
DB 242 TCVSHVCAVFIFFYPFICLSWVHRSKRSDPLPVIIANIIYLVPEVLPNPIYGVYKTKEI 301
QY 301 RORIRLRFHVATHASEP 317
DB 302 RORIRLRFHVATHASEP 318
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RESULT 10

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US-09-895-814-920
; Sequence 920, Application US/09895814
; Publication No. US20020193296A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 920
; LENGTH: 318
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-895-814-920
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Query Match 99.8%; Score 1614; DB 10; Length 318;
Best Local Similarity 99.7%; Pred. No. 1,2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPNGNSESATYFIIIGLPGLEAOFWLAFLCSYLVANIGNTIIYVTRTHSHLP 60
DB 2 MDPNGNSESATYFIIIGLPGLEAOFWLAFLCSYLVANIGNTIIYVTRTHSHLP 61
QY 61 MYIFCLMSGIDILISTSSMPKMLAIFWNSSTIIQFDACILQMFALHSLSGNESTVLLAM 120
DB 62 MYIFCLMSGIDILISTSSMPKMLAIFWNSSTIIQFDACILQMFALHSLSGNESTVLLAM 121
QY 121 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 180
DB 122 AFRRYVAICHPRLHATVLTLPRTVKIGVAAVRGAAIMAPLPVFIKQLPFCRSNIIISHSY 181
QY 181 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
DB 182 CLHODVWKLACDDIRVVNVVGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
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Tue Feb 10 06:04:27 2004

us-10-017-066a-2.rapb

Page 6

QY 241 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 300
DB 242 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 301
QY 301 RORILRLFHVATHASEP 317
DB 302 RORILRLFHVATHASEP 318

RESULT 11
US-09-966-459A-2
; Sequence 2, Application US/09966459A
; Publication No. US2003002237A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J.N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C.S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNAK, M.G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPMY4,
; FILE REFERENCE: D0039NP
; CURRENT APPLICATION NUMBER: US/09/966,459A
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,833
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,776
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/305,351
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,202
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-459A-2

Query Match 99.8%; Score 1614; DB 11; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 120
DB 2 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 121
QY 61 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 120
DB 62 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 121
QY 121 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHSY 180
DB 122 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHSY 181
QY 181 CLHODVWKLACDDIRVNVVGLIIVISAIGLDSILISFSYLLIKTVLGLTREQAQAFG 240
DB 182 CLHODVWKLACDDIRVNVVGLIIVISAIGLDSILISFSYLLIKTVLGLTREQAQAFG 241
QY 241 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 300
DB 242 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 301
QY 301 RORILRLFHVATHASEP 317
DB 302 RORILRLFHVATHASEP 318

RESULT 12

US-09-804-291-91
; Sequence 91, Application US/09804291
; Publication No. US2003008059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0278005
; CURRENT APPLICATION NUMBER: US/09/804,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 91
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-291-91

Query Match 99.8%; Score 1614; DB 11; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 120
DB 2 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 121
QY 61 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 120
DB 62 MYIFCLMSSGIDILISTSSMPKMLAIFWENSTTIQFDACLLQFAHISGMESTVLLAM 121
QY 121 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHSY 180
DB 122 AFDRYVAICPLRHATVLTLPRTYKIGVAAVVRGALMAPLPVFIKQLPFCRSNIIISHSY 181
QY 181 CLHODVWKLACDDIRVNVVGLIIVISAIGLDSILISFSYLLIKTVLGLTREQAQAFG 240
DB 182 CLHODVWKLACDDIRVNVVGLIIVISAIGLDSILISFSYLLIKTVLGLTREQAQAFG 241
QY 241 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 300
DB 242 TCVSHVCAVFIFVYVFIQLSMVHRFSKRSDSPPLVILANTYLLVPPVLPVYGVKTKKEI 301
QY 301 RORILRLFHVATHASEP 317
DB 302 RORILRLFHVATHASEP 318

RESULT 13
US-10-017-161-868
; Sequence 868, Application US/10017161
; Publication No. US2003014366A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 868
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-161-868

Query Match 99.8%; Score 1614; DB 12; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 60
DB 2 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 61
QY 61 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 120
DB 62 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 121
QY 121 AFDRIYALCHPLRHATVTLPRYTKIGVAAVVRGALMLAPLPIFKQLPFCRSNIIISHSY 180
DB 122 AFDRIYALCHPLRHATVTLPRYTKIGVAAVVRGALMLAPLPIFKQLPFCRSNIIISHSY 181
QY 181 CLHQDVAKLACDDIRNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
DB 182 CLHQDVAKLACDDIRNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
QY 241 TCVSHVCANFIYVPFIIIGLSMVRFSKRDSPPLVILANIIYLVPLNPIYGVYKTEI 300
DB 242 TCVSHVCANFIYVPFIIIGLSMVRFSKRDSPPLVILANIIYLVPLNPIYGVYKTEI 301
QY 301 RORILRLFHVAATHASEP 317
DB 302 RORILRLFHVAATHASEP 318

RESULT 14
US-10-144-678A-920
Sequence 920, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelley, Yaser A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals Y de Bassols, Carlotia
APPLICANT: Roy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-920

Query Match 99.8%; Score 1614; DB 12; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 60
DB 2 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 61
QY 61 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 120
DB 62 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 121
QY 121 AFDRIYALCHPLRHATVTLPRYTKIGVAAVVRGALMLAPLPIFKQLPFCRSNIIISHSY 180
DB 122 AFDRIYALCHPLRHATVTLPRYTKIGVAAVVRGALMLAPLPIFKQLPFCRSNIIISHSY 181
QY 181 CLHQDVAKLACDDIRNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 240
DB 182 CLHQDVAKLACDDIRNVVYGLIIVISAIGDLSLISFSYLLIKTVLGLTREAOAKAFG 241
QY 241 TCVSHVCANFIYVPFIIIGLSMVRFSKRDSPPLVILANIIYLVPLNPIYGVYKTEI 300
DB 242 TCVSHVCANFIYVPFIIIGLSMVRFSKRDSPPLVILANIIYLVPLNPIYGVYKTEI 301
QY 301 RORILRLFHVAATHASEP 317
DB 302 RORILRLFHVAATHASEP 318

RESULT 15
US-10-294-025-920
Sequence 920, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 920
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-025-920

Query Match 99.8%; Score 1614; DB 12; Length 318;
Best Local Similarity 99.7%; Pred. No. 1.2e-149;
Matches 316; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 60
DB 2 MVDPNNGESSATYFIIIGLPGLEAOFWLAFLCSYLLAVGNLTIIYVRETHSLHEP 61
QY 61 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 120
DB 62 MYIFLCMLSGIDILISTSSMPKMLAFWENSTTIQDACLQIIFAHSLSGMESTVLLAM 121

Qy 121 AFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGAMAPLPVFIKQLPFCRSNIIISHSY 180
Db 122 AFDRYVAICHPLRHATVLTLPRTKIGVAAVVRGAMAPLPVFIKQLPFCRSNIIISHSY 181
Qy 181 CIHODVKKLACDDIRRVNVVGLIVISAGLDSLITSFSYLLIKTVLGITREAOAKAFG 240
Db 182 CIHODVKKLACDDIRRVNVVGLIVISAGLDSLITSFSYLLIKTVLGITREAOAKAFG 241
Qy 241 TCVSHVCAVFIFFYPFIGLSVHRFSKRDSPLPVILANIYLLVPPYLPNIYVGVKTKEI 300
Db 242 TCVSHVCAVFIFFYPFIGLSVHRFSKRDSPLPVILANIYLLVPPYLPNIYVGVKTKEI 301
Qy 301 RQRLRLPHVATHASEP 317
Db 302 RQRLRLPHVATHASEP 318

Search completed: February 9, 2004, 16:30:47
Job time : 35 secs


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Db      1 MVDNGNSSATYITLLGLPGLBEAQFWLAFPLCSLYLIVLGNLTITIVYVREHSLHEP 60
Qy      61 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIQPDACILQIFAIHSLSGMESTVLLAM 120
Db      61 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIQPDACILQIFAIHSLSGMESTVLLAM 120
Qy      121 AFDRYVAICHPRLRAVTLTPRYTKIGVAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
Db      121 AFDRYVAICHPRLRAVTLTPRYTKIGVAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
Qy      181 CLHODVWKLACDDIRVNVVYGLIYISALIGDLSILISFSYLLILKTVLGLTREAOAKAFG 240
Db      181 CLHODVWKLACDDIRVNVVYGLIYISALIGDLSILISFSYLLILKTVLGLTREAOAKAFG 240
Qy      241 TCVSHVCAVFIYYVFFIGLSVWHRFSKRDSPLPYIANTIVLVPVLPNPIYGVTKKEI 300
Db      241 TCVSHVCAVFIYYVFFIGLSVWHRFSKRDSPLPYIANTIVLVPVLPNPIYGVTKKEI 300
Qy      301 RQRIILRLFHVATPHASEP 317
Db      301 RQRIILRLFHVATPHASEP 317

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RESULT 2

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ID      08VGZ7      PRELIMINARY;      PRT;      317 AA.
AC      08VGZ7;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Olfactory receptor MOR18-1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AY072993; AAL60656.1; -
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHDOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
SQ      SEQUENCE 317 AA; 35463 MW; 5A0E59E229852534 CRC64;

```

Query Match 93.5%; Score 1512; DB 11; Length 317;
 Best Local Similarity 93.4%; Pred. No. 1.9e-126;
 Matches 295; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

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Qy      1 MVDNGNSSATYITLLGLPGLBEAQFWLAFPLCSLYLIVLGNLTITIVYVREHSLHEP 60
Db      1 MVDNGNSSATYITLLGLPGLBEAQFWLAFPLCSLYLIVLGNLTITIVYVREHSLHEP 60
Qy      61 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIQPDACILQIFAIHSLSGMESTVLLAM 120
Db      61 MYIFLCMLSGIDILISTSSMPKMLAIFWNSSTIQPDACILQIFAIHSLSGMESTVLLAM 120
Qy      121 AFDRYVAICHPRLRAVTLTPRYTKIGVAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
Db      121 AFDRYVAICHPRLRAVTLTPRYTKIGVAVVRGAALMAPLPVFIKQLPFCRSNIIISHSY 180
Qy      181 CLHODVWKLACDDIRVNVVYGLIYISALIGDLSILISFSYLLILKTVLGLTREAOAKAFG 240
Db      181 CLHODVWKLACDDIRVNVVYGLIYISALIGDLSILISFSYLLILKTVLGLTREAOAKAFG 240

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Qy      241 TCVSHVCAVFIYYVFFIGLSVWHRFSKRDSPLPYIANTIVLVPVLPNPIYGVTKKEI 300
Db      241 TCVSHVCAVFIYYVFFIGLSVWHRFSKRDSPLPYIANTIVLVPVLPNPIYGVTKKEI 300
Qy      301 RQRIILRLFHVATPHASE 316
Db      301 RQRIILRLFHVATPHASE 316

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RESULT 3

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ID      08VAV9      PRELIMINARY;      PRT;      320 AA.
AC      08VAV9;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Olfactory receptor MOR18-2 (Prostate-specific G protein-coupled
DE      receptor RALc).
GN      OLF78.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AY073011; AAL60674.1; -
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRHDOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
SQ      SEQUENCE 320 AA; 35577 MW; 7161ACAF4328959 CRC64;

```

Query Match 60.9%; Score 985; DB 11; Length 320;
 Best Local Similarity 59.8%; Pred. No. 1.3e-79;
 Matches 183; Conservative 53; Mismatches 68; Indels 2; Gaps 2;

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Qy      7 NESSATYIFILIGLGLBEAQFWLAFPLCSLYLIVLGNLTITIVYVREHSLHEPMYFLC 66
Db      5 NEHTATFLIGLIGLGLBEAQFWLAFPLCSLYLIVLGNLTITIVYVREHSLHEPMYFLC 63
Qy      67 MLSGIDILISTSSMPKMLAIFWNSSTIQPDACILQIFAIHSLSGMESTVLLAMAFPRVY 126

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Db      64 MAAIADLALSTSTMPKILALFMFDSREITFDACLAOMFPIHLSIAESTILLAMAFDRYV 123
Qy      127 AICHPLRHATVTLPRYTKIGVAAYRGALMALPVLVFIKOLPECRSNTLSHCYCLHODV 186
Db      124 AICHPLRHAAVNLNTYVQIGWALVRGSLFFPPLILIKRLAFCHSNVLSHSCYCHODV 183
Qy      187 MKIACDDIRVNVVYGLVIVISAIGLDSLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
Db      184 MKIAYDTLPNVVYGLTALILVMGVMEFISLSYFLIIRTVLQPEKSRAPAFGTCVSH 243
Qy      246 VCAVFIFYPFIFGLSMVHRFSKRSDSPLVILANITLVLPVLANIYVGVTKREKRL 305
Db      244 ISVVALFVYVPLIGLSVVRHFGNSLDPIVHLMGDVYLLPVPINPIYGAKTQIRTVL 303
Qy      306 RLPHVA 311
Db      304 AMFKIS 309

```

RESULT 4

```

ID      Q8VF09      PRELIMINARY;      PRT;      322 AA.
AC      Q8VF09;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Olfactory receptor MOR18-3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10990;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhang X., Firestein S.J.;
RT      "The olfactory receptor gene superfamily of the mouse.";
RL      Nat. Neurosci. 0:0-0(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Adams M.;
RT      Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL      EMBL: AY073732; AAL61395.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor.
SQ      SEQUENCE 322 AA; 35612 MW; D40302782D4B2FBE CRC64;

```

```

Query Match      59.7%; Score 965.5; DB 11; Length 322;
Best Local Similarity 59.0%; Pred. No. 7.3e-78;
Matches 181; Conservative 57; Mismatches 66; Indels 3; Gaps 3;

```

```

Qy      4  PNGNSSATYFILGLPGL-EEAQFWLAFLPCLSLILAVLGNLTITIVYREHSHLHPMT 62
Db      12  PNGSLHPRVFLVGLPGISKIHFWLAFPLCFEVAATLGNLAIIFIRERRLHEMY 71
Qy      63  IFLCMISGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMSYVLLAMAF 122
Db      72  LFLAALSTIDLVSSVMPKMSLFLTGIEIEFICLTQMFILHALSAMSAVLLAMAF 131
Qy      123  DRYVALCHPLRHATVTLPRYTKIGVAAYRGALMALPVLVFIKOLPECRSNTLSHCYCL 182
Db      132  DRYVALCHPLRHASVLTGTVAKIGIASLARGFVFPPLPFLKRLSYCQTHVTHSPCL 191
Qy      183  HODVVKLACDDIRVNVVYGLVIVISAIGLDSLISFSYLLILKTVLGL-TREAQAKAFGT 241
Db      192  HODIMKLSCTDTRNVVYGLFIIISVGVDSLFIFGSIILIRAVLELSTGALLKAFNT 251
Qy      242  CVSHVCAVFIYVPTIGLSMVHRFSKRSDSPLVILANITLVLPVLANIYVGVTKYKIR 301
Db      252  CISHCAVAVFYVPLIGLSVVRHFG-GPTSLVHVIMANITVLLPVPVPIYGAKTKEIR 310

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Qy      302 ORILRLP 308
Db      311 SRVIRMP 317

```

RESULT 5

```

ID      Q8NGF3      PRELIMINARY;      PRT;      324 AA.
AC      Q8NGF3;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Seven transmembrane helix receptor.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA      Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT      "Genome-wide discovery and analysis of human seven transmembrane helix
RT      receptor genes.";
RL      Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR      EMBL: AB055855; BAC06073.1;
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW      Receptor; Transmembrane.
SQ      SEQUENCE 324 AA; 35839 MW; 52401F88565E3BD1 CRC64;

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Query Match      58.0%; Score 937.5; DB 4; Length 324;
Best Local Similarity 58.5%; Pred. No. 2.3e-75;
Matches 179; Conservative 52; Mismatches 72; Indels 3; Gaps 3;

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```

Qy      5  NNGESSATYFILGLPGL-EEAQFWLAFLPCLSLILAVLGNLTITIVYREHSHLHPMT 63
Db      15  NGMLVHAAYPLVGLIPGLPTTHFWLAFPLCFEVAATLGNLITVILIRERRLHEMYL 74
Qy      64  FFLCMISGIDILISTSSMPKMLAFWNSSTTIQPDACILQIFAHSLSGMSYVLLAMAF 123
Db      75  FLMLSTIDLVSSIMPKMSLFLMGIGIEIBENICLQMFILHALSAMSAVLLAMAF 134
Qy      124  RYVALCHPLRHATVTLPRYTKIGVAAYRGALMALPVLVFIKOLPECRSNTLSHCYCL 183
Db      135  RYVALCHPLRHASVLTGTVAKIGIASLALTRGFVFPPLPFLKRLSYCQTHVTHSPCL 194
Qy      184  QDVVKLACDDIRVNVVYGLVIVISAIGLDSLISFSYLLILKTVLGL-TREAQAKAFGT 242
Db      195  QDIMKLSCTDTRNVVYGLFIIISVGVDSLFIFGSIILIRAVLELSTGALLKAFNT 254
Qy      243  VSHVCAVFIYVPTIGLSMVHRFSKRSDSPLVILANITLVLPVLANIYVGVTKYKIR 302
Db      255  ISHCAVAVFYVPLIGLSVVRHFG-GPTSLVHVIMANITVLLPVPVPIYGAKTKEICS 313
Qy      303  RLRLP 308
Db      314  RVLQMP 319

```

RESULT 6

```

ID      Q8VH05      PRELIMINARY;      PRT;      315 AA.
AC      Q8VH05;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT      01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE      Olfactory receptor MOR10-1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


Db 68 LSMALIDGLSLCTLPVTLGI FVWGAREISHDA CFAQLFFIHCFSPLESSVLLISMAFDR 127
 QY 125 YVAICHPLRHATVTLTPRVTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIILSHSYCHQ 184
 Db 128 FVAICHPLRHATVTLTPRVTKIGVLSLGRSVALIFPLPMLKRPYCGSPILSHSYCHQ 187
 QY 185 DVMKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 243
 Db 188 EVMKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 247
 QY 244 SHVCAVF-FYVYFPIGLSWHRSKRDSPLPVILANIYLVVPLNPIYVGVTKRIOR 303
 Db 248 SHICAVLLFYTPMIGLSVHFRFGKAPHLVQVWGMFVLLPFPVNIIVISVTKIQRDR 307
 QY 304 ILRLP 308
 Db 308 VTHAF 312

RESULT 9

Q8VH17 PRELIMINARY; PRT; 313 AA.
 ID Q8VH17
 AC Q8VH17;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Olfactory receptor MOR7-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AY072971; AAL6034.1; -
 DR EMBL; AY072971; AAL6034.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 313 AA; 35682 MW; 39476E03FD201D6C CRC64;

Query Match 54.2%; Score 877; DB 11; Length 313;
 Best Local Similarity 51.8%; Pred. No. 5.2e-70;

Matches 158; Conservative 72; Mismatches 73; Indels 2; Gaps 2;

QY 5 NGENESATYFIIIGPGLBEAQFWLAPLCSLYLAVGNLTIIYIVTRESLHEPMYIF 64
 Db 6 NSSLQKAFPP-LTSGQSEERHGWISIFCSIVLIVILGNLTIIHVRTDITLHEPMYIF 64
 QY 65 LCMISGIDILISTSMPKMLAIFWENSTTIQFDACLLQIPAIHSLSGMESTVILMAFDR 124
 Db 65 LAMALATDGLCLSTLPVLGIFWFDAREIGIPACFTQLFIHTLSVSSSVLLSMGFDR 124
 QY 125 YVAICHPLRHATVTLTPRVTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIILSHSYCHQ 184
 Db 125 YVAICHPLRHATVTLTPRVTKIGVLSLGRSVALIFPLPMLKRPYCGSPILSHSYCHQ 184
 QY 185 DVMKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 243
 Db 185 EVMKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 247
 QY 244 SHVCAVF-FYVYFPIGLSWHRSKRDSPLPVILANIYLVVPLNPIYVGVTKRIOR 303
 Db 248 SHICAVLLFYTPMIGLSVHFRFGKAPHLVQVWGMFVLLPFPVNIIVISVTKIQRDR 307

QY 304 ILRLP 308
 Db 308 IIRKF 309

RESULT 10

Q8VG26 PRELIMINARY; PRT; 314 AA.
 ID Q8VG26
 AC Q8VG26;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Olfactory receptor MOR14-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.;
 RT "The olfactory receptor gene superfamily of the mouse."
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.;
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AY072994; AAL6057.1; -
 DR EMBL; AY072994; AAL6057.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 314 AA; 35096 MW; 9F1016F881A040E9 CRC64;

Query Match 54.1%; Score 875.5; DB 11; Length 314;
 Best Local Similarity 52.3%; Pred. No. 7.1e-70;

Matches 162; Conservative 63; Mismatches 82; Indels 3; Gaps 2;

QY 4 PGENESSA--TFEIIIGPGLBEAQFWLAPLCSLYLAVGNLTIIYIVTRESLHEPMYIF 61
 Db 2 PGENESSA--TFEIIIGPGLBEAQFWLAPLCSLYLAVGNLTIIYIVTRESLHEPMYIF 61
 QY 62 YIFLCMLSGIDILISTSMPKMLAIFWENSTTIQFDACLLQIPAIHSLSGMESTVILMAFDR 121
 Db 62 YIFLCMLSGIDILISTSMPKMLAIFWENSTTIQFDACLLQIPAIHSLSGMESTVILMAFDR 121
 QY 122 FDRYVACHPLRHATVTLTPRVTKIGVAAYVGAALMAPLPVFIKOLPFCRSNIILSHSYCHQ 181
 Db 122 FDRYVACHPLRHATVTLTPRVTKIGVLSLGRSVALIFPLPMLKRPYCGSPILSHSYCHQ 181
 QY 182 LHDVWKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 240
 Db 182 LHDVWKLACDDIRVVNVYGLIIVISAIIGDLSLISFYLILKTIVGLTREACA-KAFITCV 240
 QY 241 TCVSHVCAVF-FYVYFPIGLSWHRSKRDSPLPVILANIYLVVPLNPIYVGVTKRIOR 300
 Db 241 TCVSHVCAVF-FYVYFPIGLSWHRSKRDSPLPVILANIYLVVPLNPIYVGVTKRIOR 300
 QY 301 RQRIILRFV 310
 Db 302 RQRIILRFV 311

RESULT 11

Q8VG22 PRELIMINARY; PRT; 314 AA.
 ID Q8VG22
 AC Q8VG22;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Olfactory receptor MOR30-1.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse.",
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072998; AAL6061.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 314 AA; 35577 MW; 718EF2F351F669 CRC64;
 Query Match 54.0%; Score 873.5; DB 11; Length 314;
 Best Local Similarity 50.2%; Pred. No. 1,1e-69;
 Matches 155; Conservative 68; Mismatches 85; Indels 1; Gaps 1;
 QY 1 MVDNGNSSATYFILGLPGLAEAPFLAFLCSLYLAVGNLTITVIREHSHLP 60
 DB 1 MVDNHSQSHLVFILGLPGLAEAPFLAFLCSLYLAVGNLTITVIREHSHLP 60
 QY 61 MYFLCMLSGIDILISTSSPKMLATFWNSTTIOFDACLLQIFAIHSLSGMSTVLLAM 120
 DB 61 MYFLALATLDIVLSSSTPKMLALHSHHEIENACLIQVFIHASSVESGLMTM 120
 QY 121 AFDRYVAICPLRAVYLTLPRTYKIGVAAVGAAALAPLVFIKQLPFCRSNLSHSY 180
 DB 121 ALDRYVAICPLRHSSILITTSVVIKGAAMVNGILMVSFPCFMVSRMFCENKVIPOSY 180
 QY 181 CLHODVWKLACDDIRVNVVGLIVITSAIGDLSLISFSLILKTYLGL-TREAQAKF 239
 DB 181 CEMNAVYKALVCASTRVNRGVLFAVSVGFDTIVISVYVILRVLRLPGEARLRAF 240
 QY 240 GTCVSHVCAVFIYVFPFGLSVHRSKRDSPLPVILANITYLVVPLVNPVYGVYKTE 299
 DB 241 GTCASHVCAVLIAYFIALFTFLTRHGHVPRVHMFANFYLLVPPMLNPIYGVYKTE 300
 QY 300 IRORIIRLF 308
 DB 301 IRDRVIRGF 309
 RESULT 12
 Q8VGZ3 PRELIMINARY; PRT; 318 AA.
 AC Q8VGZ3;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Olfactory receptor MOR10-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse.",
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072997; AAL6060.1; -
 DR InterPro; IPR001064; Crystallin.

DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 318 AA; 35593 MW; 3A9699B821087B48 CRC64;
 Query Match 54.0%; Score 873.5; DB 11; Length 318;
 Best Local Similarity 54.4%; Pred. No. 1,1e-69;
 Matches 168; Conservative 55; Mismatches 85; Indels 1; Gaps 1;
 QY 1 MVDNGNSSATYFILGLPGLAEAPFLAFLCSLYLAVGNLTITVIREHSHLP 60
 DB 1 MADNHSQSHLVFILGLPGLAEAPFLAFLCSLYLAVGNLTITVIREHSHLP 60
 QY 61 MYFLCMLSGIDILISTSSPKMLATFWNSTTIOFDACLLQIFAIHSLSGMSTVLLAM 120
 DB 61 MYFLCMLAFLADMGTLCTLPMLGIFWFKYKRTPDGCLVQWYFIHTFSAISGLVAM 120
 QY 121 AFDRYVAICPLRAVYLTLPRTYKIGVAAVGAAALAPLVFIKQLPFCRSNLSHSY 180
 DB 121 ALDRYVAICPLRAVYLTLPRTYKIGVAAVGAAALAPLVFIKQLPFCRSNLSHSY 180
 QY 181 CLHODVWKLACDDIRVNVVGLIVITSAIGDLSLISFSLILKTYLGL-TREAQAKF 239
 DB 181 CLHODVWKLACDDIRVNVVGLIVITSAIGDLSLISFSLILKTYLGL-TREAQAKF 240
 QY 240 GTCVSHVCAVFIYVFPFGLSVHRSKRDSPLPVILANITYLVVPLVNPVYGVYKTE 299
 DB 241 NTCVSHVCAVLIAYFIALFTFLTRHGHVPRVHMFANFYLLVPPMLNPIYGVYKTE 300
 QY 300 IRORIIRLF 308
 DB 301 IRKRIIOIF 309
 RESULT 13
 Q8VH01 PRELIMINARY; PRT; 317 AA.
 AC Q8VH01;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Olfactory receptor MOR19-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Zhang X., Firestein S.J.,
 RT "The olfactory receptor gene superfamily of the mouse.",
 RL Nat. Neurosci. 0:0-0(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Adams M.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY072987; AAL6060.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM Receptor.
 SQ SEQUENCE 317 AA; 35357 MW; 165BC74BC379CA7 CRC64;
 Query Match 53.3%; Score 862.5; DB 11; Length 317;
 Best Local Similarity 53.2%; Pred. No. 1e-68;
 Matches 158; Conservative 55; Mismatches 79; Indels 1; Gaps 1;
 QY 15 ILGLPGLAEAPFLAFLCSLYLAVGNLTITVIREHSHLPYIFLCMLSGIDIL 74

Db 15 LITGIGLEADVOICPILCWVYIALALNCTILVIRTTSSLSHPXYIFLSMLATDVG 74
Qy 75 ISTSNPKKALAFWENSTTIQDACLQIFAHISJSGHESTVLLAMADRYAICHPIRH 134
Db 75 LSVSTILPTLVANFELNHRDIEFHSCLTQMFHTFTSSMESALILMAFDRFAIENSLHY 134
Qy 135 AVVLTLPRTVTKIGVAAVVGALMAPLPVFKQLPFCRSNIIISHSCLHODVMKACDDI 194
Db 135 TAVLPTTRIKIGLAANVAVGWMILPILKLPFCGVILSHCYCHPDMKACGPV 194
Qy 195 RVNVVGLIVITSAIGLDSILISFVYLILKTVGL-TREAQAKAFGTCVSHVCAVFIY 253
Db 195 RVNIYIGSLVYCSFQVDSVFIIVISYILILKTVGLASGDGKLALNTCVSHIFVFIY 254
Qy 254 VPIGISMVHRFSKRDSPILANIVYLVPPVNPVYGVYKTEIRILRLFHV 310
Db 255 VPLIVLALHRRGTFSPLHVTMANLFLFPLVNPVYSLKTKQISAVCKLIFKV 311

RESULT 14

Q8VGM0 PRELIMINARY; PRT; 319 AA.

AC Q8VGM0;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Olfactory receptor MOR30-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A073034; AL60697.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 319 AA; 35988 MW; B2DB4A1465A063F CRC64;

Query Match 53.0%; Score 857.5; DB 11; Length 319;
Best Local Similarity 49.5%; Pred. No. 2,9e-68;
Matches 154; Conservative 66; Mismatches 90; Indels 1; Gaps 1;

Qy 1 WDPNGNESSATYFLLIGPGLSEAQFWLAPLCSLYLAVGNLTITYIVRTSHLHP 60
Db 6 MASNSSSVSSTFFYLIGPGLSENYQFWAFPCMYIVAVGNLTIIHRIHTLHP 65
Qy 61 MYIFLCMSGIDILISTSSMPKALAFWENSTTIQDACLQIFAHISJSGHESTVLLAM 120
Db 66 MYIFLCMSGIDILISTSSMPKALAFWENSTTIQDACLQIFAHISJSGHESTVLLAM 125
Qy 121 AFRYYAICHPLRHATVLTLPRTVTKIGVAAVVGALMAPLPVFKQLPFCRSNIIISHY 180
Db 126 ALDRYYAICHPLRHATVLTLPRTVTKIGVAAVVGALMAPLPVFKQLPFCRSNIIISHY 185
Qy 181 CHQDVMKACDDIRNVVYVGLVITSAIGLDSILISFVYLILKTVGL-TREAQAKAF 239
Db 186 CEHMAVILKVCADIRNVVYVGLVITSAIGLDSILISFVYLILKTVGL-TREAQAKAF 245
Qy 240 GTCVSHVCAVFIYVPIGISMVHRFSKRDSPILANIVYLVPPVNPVYGVYKTE 299
Db 246 GTCASHIGVILITLYIPALFTPLTHRFQGHVPRVAVHMEANVYLLVPPMLNPIIGVTRKQ 305

Qy 300 IRORIILRLFHV 310
Db 306 IRORYTRGFCV 316

RESULT 15

Q8VGM0 PRELIMINARY; PRT; 319 AA.

AC Q8VGM0;
DT 01-MAR-2002 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Olfactory receptor MOR17-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A072392; AL60655.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 319 AA; 36040 MW; D3FP2D8755FDC2F CRC64;

Query Match 53.0%; Score 857.5; DB 11; Length 319;
Best Local Similarity 52.9%; Pred. No. 2,9e-68;
Matches 163; Conservative 57; Mismatches 87; Indels 1; Gaps 1;

Qy 1 WDPNGNESSATYFLLIGPGLSEAQFWLAPLCSLYLAVGNLTITYIVRTSHLHP 60
Db 1 MASNSVSSTFFYLIGPGLSENYQFWAFPCMYIVAVGNLTIIHRIHTLHP 60
Qy 61 MYIFLCMSGIDILISTSSMPKALAFWENSTTIQDACLQIFAHISJSGHESTVLLAM 120
Db 61 MYIFLCMSGIDILISTSSMPKALAFWENSTTIQDACLQIFAHISJSGHESTVLLAM 120
Qy 121 AFRYYAICHPLRHATVLTLPRTVTKIGVAAVVGALMAPLPVFKQLPFCRSNIIISHY 180
Db 121 ALDRYYAICHPLRHATVLTLPRTVTKIGVAAVVGALMAPLPVFKQLPFCRSNIIISHY 180
Qy 181 CHQDVMKACDDIRNVVYVGLVITSAIGLDSILISFVYLILKTVGL-TREAQAKAF 239
Db 181 CHQDVMKACDDIRNVVYVGLVITSAIGLDSILISFVYLILKTVGL-TREAQAKAF 240
Qy 240 GTCVSHVCAVFIYVPIGISMVHRFSKRDSPILANIVYLVPPVNPVYGVYKTE 299
Db 241 NTGASHICAVLILYVMIGSLIYHRAKSSPRVHIFMAHITLMPVNPVNPVYKTKQ 300
Qy 300 IRORIILRL 307
Db 301 IROGIIFHL 308

Search completed: February 9, 2004, 16:25:11
Job time: 43 secs

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OM protein - protein search, using sw model

Run on: February 9, 2004, 16:18:01 ; Search time 17 Seconds
(without alignments)

876,910 Million cell updates/sec

Title: US-10-017-066a-2

Perfect score: 1617
Sequence: 1 MVDPNNESSATYFTLIGLP.....KEIRQRLRLPHVATHASEP 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	60.5	320	1 OXK2_HUMAN	O9H255 homo sapien
2	977	60.4	320	1 OXK2_RAT	O9H258 rattus norv
3	868.5	53.7	312	1 OX12_HUMAN	O9H344 homo sapien
4	806.5	49.9	314	1 OX11_HUMAN	O9H343 homo sapien
5	792.5	49.0	318	1 OXV1_HUMAN	O9H346 homo sapien
6	774.5	47.9	315	1 OXW1_HUMAN	O9H341 homo sapien
7	762	47.1	317	1 OXB2_HUMAN	O9H342 homo sapien
8	751	46.4	312	1 OXK1_HUMAN	O9H342 homo sapien
9	728.5	45.1	312	1 OXK2_HUMAN	O9H341 homo sapien
10	704	43.5	313	1 OXB6_HUMAN	O9H343 homo sapien
11	632	39.1	310	1 OXB4_HUMAN	O9H343 homo sapien
12	464	28.7	319	1 OXB2_HUMAN	O9H343 homo sapien
13	439	27.1	312	1 OXB2_HUMAN	O9H343 homo sapien
14	434.5	26.9	312	1 OXB2_HUMAN	O9H343 homo sapien
15	432.5	26.7	312	1 OXB2_HUMAN	O9H343 homo sapien
16	431.5	26.7	310	1 OXB2_HUMAN	O9H343 homo sapien
17	431.5	26.7	314	1 OXB2_HUMAN	O9H343 homo sapien
18	430.5	26.6	314	1 OXB2_HUMAN	O9H343 homo sapien
19	428.5	26.5	311	1 OXB2_HUMAN	O9H343 homo sapien
20	428	26.5	317	1 OXB2_HUMAN	O9H343 homo sapien
21	427.5	26.4	314	1 OXB2_HUMAN	O9H343 homo sapien
22	427	26.4	312	1 OXB2_HUMAN	O9H343 homo sapien
23	426	26.3	315	1 OXB2_HUMAN	O9H343 homo sapien
24	425.5	26.3	314	1 OXB2_HUMAN	O9H343 homo sapien
25	425.5	26.3	320	1 OXB2_HUMAN	O9H343 homo sapien
26	424.5	26.3	315	1 OXB2_HUMAN	O9H343 homo sapien
27	423.5	26.2	312	1 OXB2_HUMAN	O9H343 homo sapien
28	423.5	26.2	321	1 OXB2_HUMAN	O9H343 homo sapien
29	421	26.0	317	1 OXB2_HUMAN	O9H343 homo sapien
30	421	26.0	317	1 OXB2_HUMAN	O9H343 homo sapien
31	420.5	26.0	312	1 OXB2_HUMAN	O9H343 homo sapien
32	420.5	26.0	313	1 OXB2_HUMAN	O9H343 homo sapien
33	418	25.9	311	1 OXB2_HUMAN	O9H343 homo sapien

ALIGNMENTS

34	416.5	25.8	314	1 OXA3_HUMAN	P58181 homo sapien
35	415.5	25.7	312	1 OLF4_CHICK	P37070 gallus gall
36	413.5	25.6	311	1 O2J3_HUMAN	O76001 homo sapien
37	413	25.5	312	1 O1D2_HUMAN	P34982 homo sapien
38	412.5	25.5	318	1 OLF1_CHICK	P37067 gallus gall
39	411.5	25.4	311	1 O8B8_HUMAN	O15620 homo sapien
40	411	25.4	311	1 OLF1_CANFA	O95154 canis fami
41	409.5	25.3	313	1 O2B6_HUMAN	P58173 homo sapien
42	409.5	25.3	313	1 O2B6_HUMAN	P32366 rattus norv
43	407.5	25.2	318	1 OLF3_CHICK	P37069 gallus gall
44	407	25.2	313	1 OLF3_CHICK	P30955 canis fami
45	407	25.2	318	1 OLF3_CHICK	O94499 homo sapien

RESULT 1	OXK2_HUMAN	STANDARD;	PRT;	320 AA.
ID	OXK2_HUMAN			
AC	O9H255;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Olfactory receptor 51b2 (prostate specific G-protein coupled receptor) (HPRAD).			
GN	OR51B2 OR PSGR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21002538; PubMed=1118034;			
RA	Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugan N.,			
RA	Seetheram I.A., Zou Z., Srikanth V., Augustus M., Roach S.,			
RA	Carter K., McLeod D.G., Moul J.W., Sopper D., Srivastava S.,			
RT	"PSGR, a novel prostate-specific gene with homology to a G			
RT	protein-coupled receptor, is overexpressed in prostate cancer."			
RL	Cancer Res. 60:6568-6572(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Xia C., Ma W., Liu M.,			
RT	"Identification of a prostate-specific G-protein coupled receptor			
RT	(PSGR) that interacts with G alpha subunit in yeast two hybrid			
RT	assay."			
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21564169; PubMed=11707321;			
RA	Yuan T.T., Toy P., McLary J.A., Lin R.J., Miyamoto N.G.,			
RA	Kretschmer P.J.,			
RT	"Cloning and genetic characterization of an evolutionarily conserved			
RT	human olfactory receptor that is differentially expressed across			
RT	species."			
RL	Gene 278:41-51(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	TRISUB=Prostate;			
RA	MEDLINE=22388257; PubMed=1247932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,			
RA	Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA	Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Phley J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			


```

QY 7 NESSATYFLLIGLPGLEENQFWLAPPLCSLYIANVGNLTIIYVTEHSHHEPMYFLC 66
DB 5 NETHAT-PELIGIPGLEENHFWGFLPSMAVALFGICIVFIRKTRSRSHAPYFLC 63
QY 67 MMSGIDILISTSSMPKMLAFWFNSTTIOFDACLIQIFAHSLSGMESTVLLAMAFDRYV 126
DB 64 MMLAIDILISTSSMPKMLAFWFNSTTIOFDACLIQIFAHSLSGMESTVLLAMAFDRYV 123
QY 127 AICHPRLHATVITLPRVTYKIGVAAYVRGAALMAPLPVFIKOLPFCRSNIIISHSYCLHODV 186
DB 124 AICHPRLHATVITLPRVTYKIGVAAYVRGAALMAPLPVFIKOLPFCRSNIIISHSYCLHODV 183
QY 187 MMLACDIDIRVNVVYGLIVISAIGLDSLSISFYSLIILKTVIGL-TREAAKAFGTGVSH 245
DB 184 MMLAIDILISTSSMPKMLAFWFNSTTIOFDACLIQIFAHSLSGMESTVLLAMAFDRYV 243
QY 246 VCAVFIFVYVPTGLSMVHRFSKRDSPFLVILANTYLLVPVLANIVYGVKTEIRORIL 305
DB 244 IGVVLAFFVYPLIGLSVHRFGNSLDPIYHVMGDVYLLPVIINIIYGAKTKQIRTVL 303
QY 306 RLEHVA 311
DB 304 AMFKIS 309

RESULT 3
OX12_HUMAN STANDARD; PRT; 312 AA.
AC 09H343;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Olfactory receptor 5112 (HORS/Beta12).
GN OR5112.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=20570519; PubMed=11121057;
RA Bulger M., Bender M.A., van Doornink J.H., Wertman B., Farrell C.M.,
RA Felsenfeld G., Groudine M., Hardison R.;
RT "Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta-globin gene
RT clusters."
RT Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; AF137396; AAG41678.1; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004984; P:olfactory receptor activity; NAS.
DR GO; GO:0007608; P:olfactory receptor activity; NAS.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm1.1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KM Multigene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 49 1 (POTENTIAL).

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FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 294 7 (POTENTIAL).
FT DOMAIN 295 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 312 AA; 35002 MW; F17CD16C95FD1AF6 CRC64;

Query Match 53.7%; Score 868.5; DB 1; Length 312;
Best Local Similarity 53.6%; Pred. No. 4.5e-60;
Matches 163; Conservative 51; Mismatches 89; Indels 1; Gaps 1;

QY 7 NESSATYFLLIGLPGLEENQFWLAPPLCSLYIANVGNLTIIYVTEHSHHEPMYFLC 66
DB 5 NETHAT-PELIGIPGLEENHFWGFLPSMAVALFGICIVFIRKTRSRSHAPYFLC 64
QY 67 MMSGIDILISTSSMPKMLAFWFNSTTIOFDACLIQIFAHSLSGMESTVLLAMAFDRYV 126
DB 65 MMSGIDILISTSSMPKMLAFWFNSTTIOFDACLIQIFAHSLSGMESTVLLAMAFDRYV 124
QY 127 AICHPRLHATVITLPRVTYKIGVAAYVRGAALMAPLPVFIKOLPFCRSNIIISHSYCLHODV 186
DB 125 AICHPRLHATVITLPRVTYKIGVAAYVRGAALMAPLPVFIKOLPFCRSNIIISHSYCLHODV 184
QY 187 MMLACDIDIRVNVVYGLIVISAIGLDSLSISFYSLIILKTVIGL-TREAAKAFGTGVSH 245
DB 185 MMLACDIDIRVNVVYGLIVISAIGLDSLSISFYSLIILKTVIGL-TREAAKAFGTGVSH 244
QY 246 VCAVFIFVYVPTGLSMVHRFSKRDSPFLVILANTYLLVPVLANIVYGVKTEIRORIL 305
DB 245 IGVVLAFFVYVPTGLSMVHRFSKRDSPFLVILANTYLLVPVLANIVYGVKTEIRORIL 304
QY 306 RLEHVA 309
DB 305 RMFH 308

RESULT 4
OX11_HUMAN STANDARD; PRT; 314 AA.
AC 09H343;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Olfactory receptor 5111 (HORS/Beta11).
GN OR5111.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=20570519; PubMed=11121057;
RA Bulger M., Bender M.A., van Doornink J.H., Wertman B., Farrell C.M.,
RA Felsenfeld G., Groudine M., Hardison R.;
RT "Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta-globin gene
RT clusters."
RT Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC EMBL, AF137396; AAG41679.1; -
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004984; F:olfactory receptor activity; NAS.
 DR GO; GO:0007608; P:olfaction; NAS.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 27
 FT TRANSMEM 26 51
 FT DOMAIN 52 59
 FT TRANSMEM 60 81
 FT DOMAIN 82 102
 FT TRANSMEM 103 122
 FT DOMAIN 123 141
 FT TRANSMEM 142 160
 FT DOMAIN 161 197
 FT TRANSMEM 198 221
 FT DOMAIN 222 238
 FT TRANSMEM 239 261
 FT DOMAIN 262 276
 FT TRANSMEM 277 296
 FT DOMAIN 297 314
 FT DISULFID 99 191
 SQ SEQUENCE 314 AA; 35483 MW; 08340AD79CB94911 CRC64;

Query Match 49.9%; Score 806.5; DB 1; Length 314;
 Best Local Similarity 48.4%; Pred. No. 2.7e-55;
 Matches 150; Conservative 66; Mismatches 93; Indels 1; Gaps 1;

QY 1 MVDNNGESSATYFLLIGLPGLEAOFMLAFPLCSLYLAIVGNLTIIYVTHESLHP 60
 DB 1 MGLNGPFPAPATLQLGIPGIQGLTWTALFCILIMISIVGNLSILTVWEPLHOP 60
 QY 61 MYFLCMTSGIDILISTSSVPMALAFWNSSTIQDACLQIFAIHSLSGNESTVLAM 120
 DB 61 MYFLSLALNDLGVSPSTLPVISTFCFVYHVAFNACLVQMFHTFSFVESGILLAM 120
 QY 121 AEDRYVALCHPLRHATVLTLPRTKIGVAAYVGAALMAPLPVFQQLPFGCSNLSH 180
 DB 121 SLDRFVALCPPLVYVLTNRLIANGLGLTSTFTLPPFPVVRRLPFCGKGNVLSHY 180
 QY 181 CLHQDVAKLACDDIRVNVVYGLVITISALGLDLSLISFSLILKTVLG-LTREAOAKAF 239
 DB 181 CLHPDLKVAACGDIHVNIVGLVITFTYGMDSFTLLSVALIKRAMLVITISQEQRLKAL 240
 QY 240 GTGVSHVCAVFYVPPIGLSMWRHRSKRDSPLPILANTILYVPPVLANPVIYGYKYE 299
 DB 241 NTGMSHCALVALYVPLIAVSMIRFKASAPVAVHVMNSVYLFPVPMNPITISYKYE 300
 QY 300 IRORIILRFH 309
 DB 301 IRKGIILKFFH 310

RESULT 5
 ID OYDI HUMAN STANDARD; PRT; 318 AA.
 AC O9H346;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 52D1 (HORS'beta14).

GN OR52D1.
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
 OC Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570519; PubMed=1121057;
 RA Bulger M., Bender M.A., van Doornink J.H., Wertman B., Farrell C.M.,
 RA Felsenfeld G., Grondine M., Hardison R.;
 RT "Comparative structural and functional analysis of the olfactory
 RT receptor genes flanking the human and mouse beta-globin gene
 RT clusters";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL, AF137396; AAG41676.1; -
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0004984; F:olfactory receptor activity; NAS.
 DR GO; GO:0007608; P:olfaction; NAS.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28
 FT TRANSMEM 29 52
 FT DOMAIN 53 60
 FT TRANSMEM 61 82
 FT DOMAIN 83 103
 FT TRANSMEM 104 123
 FT DOMAIN 124 142
 FT TRANSMEM 143 161
 FT DOMAIN 162 198
 FT TRANSMEM 199 222
 FT DOMAIN 223 239
 FT TRANSMEM 240 262
 FT DOMAIN 263 278
 FT TRANSMEM 279 298
 FT DOMAIN 299 318
 FT DISULFID 100 192
 FT CABOYHD 5 5
 SQ SEQUENCE 318 AA; 35121 MW; 178968087D613CB2 CRC64;

Query Match 49.0%; Score 792.5; DB 1; Length 318;
 Best Local Similarity 46.2%; Pred. No. 3.3e-54;
 Matches 145; Conservative 71; Mismatches 93; Indels 5; Gaps 4;

QY 1 MVDN--GNSSATYFLLIGLPGLEAOFMLAFPLCSLYLAIVGNLTIIYVTHESLH 58
 DB 1 MSDNLSDNHLPDFF-LTGLPGLEAHFMAIAPFCMYVALVGNALILVIAAMDALH 59
 QY 59 EPMYFLCMTSGIDILISTSSVPMALAFWNSSTIQDACLQIFAIHSLSGNESTVL 118
 DB 60 APMYLFLCLSLTDIALSSTVPMALILWLHAGEISFGGLAQMFVSHIYALSSILL 119
 QY 119 AMAEDRYVALCHPLRHATVLTLPRTKIGVAAYVGAALMAPLPVFQQLPFGCSNLSH 178
 DB 120 AMAEDRYVALCHPLRHTIILNHAIVGIGVGLFRSAIYVSPFILLRLPYGCHRWTH 179
 QY 179 SYCLHQDVAKLACDDIRVNVVYGLVITISALGLDLSLISFSLILKTVLG-LTREAOAK 237

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Db      180  TICEHNGIARLACANTIVAYGLTVALLMGLDILIAISGFIHAVFHLPSHDQHK 239
Qy      236  AFGTCVSHVCAVFIYVPPFISGMVHRSFKRR-DSPLEVIATANIYLVAPVIANPIYGVK 296
Db      240  ALSTGSHIGIILVFIYPAFSPFLTHRFQGHVHPGHVHILANLVVAPVIANPIYAR 299
Qy      297  TFEIRORILRFRV 310
Db      300  TFEIRSRILKILHL 313

RESULT 6
OXM1_HUMAN
ID      OXM1_HUMAN      STANDARD;      PRT;      315 AA.
AC      Q9H341;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Olfactory receptor 51M1 (HORS/beta7).
GN      OR51M1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN      [1] TaxID=9606;
RP      MEDLINE=20570519; PubMed=1121057;
RA      Bulger M., Bender M.A., van Doorninck J.H., Westman B., Farrell C.M.,
RT      Feltsenfeld G., Groudine M., Hardison R.;
RT      "Comparative structural and functional analysis of the olfactory
RT      receptor genes flanking the human and mouse beta-globin gene
RT      clusters.";
RL      Proc. Natl. Acad. Sci. U.S.A. 97:14560-14566(2000).
CC      - FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC      - SUBCELLULAR LOCATION: Integral membrane protein.
CC      - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      - This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      EMBL: AF137396; AAG41681.1; ALT INIT.
DR      GO: GO:0016021; C:intracellular receptor activity; NAS.
DR      GO: GO:0006984; F:olfactory receptor activity; NAS.
DR      GO: GO:0007608; P:olfaction; NAS.
DR      InterPro: IPR00276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm.1.1.
DR      PRINTS: PR00237; GPCR_RHODOPSIN.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR      G-protein coupled receptor; Transmembrane; Glycoprotein;
KM      Multigene family; Olfaction.
FT      DOMAIN 1 26
FT      TRANSMEM 27 50
FT      DOMAIN 51 58
FT      TRANSMEM 59 80
FT      DOMAIN 81 101
FT      TRANSMEM 102 121
FT      DOMAIN 122 140
FT      TRANSMEM 141 159
FT      DOMAIN 160 196
FT      TRANSMEM 197 220
FT      DOMAIN 221 237
FT      TRANSMEM 238 260
FT      DOMAIN 261 275
FT      TRANSMEM 276 295
FT      DOMAIN 296 315
FT      DISULFID 98 190
FT      BY SIMILARITY.

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FT      CARBOHYD 5 5 N-LINKED (GLCNAC..) (POTENTIAL).
SQ      SEQUENCE 315 AA; 35462 MW; DC19D2F5456D2005 CRC64;
Qy      Query March 47.9%; Score 774.5; DB 1; Length 315;
Db      Best local similarity 47.5%; Pred. No. 7.9e-53;
Matches 140; Conservative 65; Mismatches 89; Indels 1; Gaps 1;
Qy      14  FILIGLPGLEBAQFWLAFPLCSLYLLAVLGNLTIVYVTRSHLHPMYIFLCMLSGIDI 73
Db      13  FYLTSPFGLGEGIKHWFIFPFPMYVAVLSGNCPIILIKTNPRPLHPMYLLSLATDL 72
Qy      74  LISTSMPEKMLAFMNSNTTIQFDACLLQIPAHISGNESTYLAADRYVAICHPR 133
Db      73  GLCVSTLPPTMGTFMWSOSIFGACQIMFCHSHSPSSSVLWMSDFRFAICHPR 132
Qy      134  HATVLTLPVYTKIGVAAYVGAALMAPLVPFIKQLPFCRSNIIISHSYCLHODVMKLACDD 193
Db      133  YSVIITIGQVVRAGLIVIRGPVATIPVLLKAPFGCSVYLSHFCLEHGVQLACDD 192
Qy      194  IRNVVYGLIVITSAIGLDSLISFSYLLIKTVAGL-TREAQAKFGTCVSHVCAVFIF 252
Db      193  TTFNNLYGLMVVVFYTWLDELVALSYGLILHTVAGLASQEEQRAFOQTARCAVLVF 252
Qy      253  YVPFISGMVHRSFKRRDSPLEVIATANIYLVAPVIANPIYGVKTEIRORILRL 307
Db      253  FVPMGLSLVHRGKAPPAIHLMANVLFVPMPLNPITISIKTKIHRALIKL 307

RESULT 7
OYB2_HUMAN
ID      OYB2_HUMAN      STANDARD;      PRT;      317 AA.
AC      Q96RD2;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Olfactory receptor 52B2.
GN      OR52B2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN      [1] TaxID=9606;
RP      SEQUENCE OF 70-287 FROM N.A.
RA      Fuchs T., Malecova B., Jinhart C., Sharan R., Kren M., Herzog R.,
RT      Smullevich D., Elkon R., Steinfath M., O'Brien J.K., Radejof U.,
RT      Lehrsach H., Olander Z., Glusman G., Lancel D., Shamir R.;
RT      "DEFOG: a practical scheme for deciphering families of genes.";
RL      Submitted (Jun-2001) to the EMBL/Genbank/DBJ databases.
CC      - FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC      - SUBCELLULAR LOCATION: Integral membrane protein.
CC      - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      - This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL: AF399505; AAK94990.1; -
DR      InterPro: IPR00276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm.1.1.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR      PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR      G-protein coupled receptor; Transmembrane; Glycoprotein;
KM      Multigene family; Olfaction.
FT      DOMAIN 1 27
FT      TRANSMEM 28 51
FT      DOMAIN 52 59
FT      TRANSMEM 60 81
FT      DOMAIN 82 102
FT      TRANSMEM 103 122
FT      BY SIMILARITY.

```

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR,
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update).

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 51B2 (HORS/Beta3).
 GN OR51B2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RX MEDLINE=9238494; PubMed=10220430;
 RA Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,
 RA Bulger M.A., Palsenfeld G., Axel R., Groudine M.,
 RT "Conservation of sequence and structure flanking the mouse and human
 RT beta-globin loci: the beta-globin genes are embedded within an array
 RT of odorant receptor genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134(1999).
 RN [2]
 RP ERRATUM.
 RA Bulger M., van Doorninck J.H., Saitoh N., Telling A., Farrell C.,
 RA Bulger M.A., Palsenfeld G., Axel R., Groudine M.,
 RL Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307(1999).
 RN [3]
 RP SEQUENCE OF 66-283 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharran R., Khen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radelof U.,
 RA Lehrach H., Olander Z., Glusman G., Lancel D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes."
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF137396; AAK94925.2; -
 CC EMBL: AF137396; AAK94925.2; -
 CC Gene: HGNC:14703; OR51B2.
 CC GO: GO:0016021; C: integral to membrane; NAS.
 CC GO: GO:0004984; F: olfactory receptor activity; NAS.
 CC GO: GO:0007608; P: olfaction; NAS.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR000237; GPCR_Rhodopsn.
 CC PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 CC PROSITE: PS00237; G-PROTEIN RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Olfaction.
 CC FT DOMAIN 1 23
 CC FT TRANSMEM 24 47
 CC FT DOMAIN 48 55
 CC FT TRANSMEM 56 77
 CC FT DOMAIN 78 98
 CC FT TRANSMEM 99 118
 CC FT DOMAIN 119 137
 CC FT TRANSMEM 138 156
 CC FT DOMAIN 157 193
 CC FT TRANSMEM 194 217
 CC FT DOMAIN 218 234
 CC FT TRANSMEM 235 257
 CC FT DOMAIN 258 272
 CC FT TRANSMEM 273 292
 CC FT DOMAIN 293 312
 CC FT TRANSMEM 312 329
 CC FT DISULFID 95 187
 CC FT CARBOHYD 4 4
 CC SEQUENCE 312 AA, 3553 MW, 60116026778EDD CRC64;
 Query Match 45.1%; Score 728.5; DB 1; Length 312;

Best Local Similarity 44.1%; Pred. No. 2,7e-49;
 Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1;

QY 10 SATYFLLGPGLEEAQFPLAPLCGLVAVGNTLIYVTEHSHEPKYIFLCMS 69
 Db 6 TAAPFLTGPPGLEAAHMTSIFFEVYCTILGNMELLILHDSLHEPMYFPLTMA 65
 QY 70 GIDILSTSSMPKMLAIFWENSTTIQDACLQIFAIHSISGMESTVLLAMAPRYAIC 129
 Db 66 GTDLMTVLTMTPTVMGLWNVNREISSVCGFLQAYFIHSISVSGSLAMAYDRFAIR 125
 QY 130 HPLRHAIVLTPRYTIGVAAVVRGALAPLDPVFKQLPFCNSNLSHSCYCHQVMTL 189
 Db 126 NPLRYASIFNTNTVIALGVGVFLRGVSLIPVLLRFSFSCKSHVITRAFCIQEIMRL 185
 QY 190 ACCDIRNVVYGLVILISAIGLDSLISPSYLLIKTVLGL-TREDAQKAFGTGSHVCA 248
 Db 186 ACADITFNRLPYVILLSTIFDLSLILPSYLLILMTVIGAGGERAKALNTCISHSC 245
 QY 249 VFIFFYPIFLSVNHRSPKRRDSPVLITANLYLVPLNPIVGVKTEIKRILRL 307
 Db 246 VLIFFYVWGLTFPIYRFGKNVPEVHIMSXYIFLEPPILMNPVYSIKTKIQYGIIRL 304

RESULT 10

OYE6_HUMAN STANDARD; PRT; 313 AA.

AC Q36RD3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Olfactory receptor 52B6.
 GN OR52B6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 70-287 FROM N.A.
 RA Fuchs T., Malecova B., Linhart C., Sharran R., Khen M., Herwig R.,
 RA Shmulevich D., Elkon R., Steinbach M., O'Brien J.K., Radelof U.,
 RA Lehrach H., Olander Z., Glusman G., Lancel D., Shamir R.;
 RT "DEFOG: a practical scheme for deciphering families of genes."
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: AF393504; AAK94989.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 CC PROSITE: PS00237; G-PROTEIN RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC Multigene family; Olfaction.
 CC FT DOMAIN 1 27
 CC FT TRANSMEM 28 51
 CC FT DOMAIN 52 59
 CC FT TRANSMEM 60 81
 CC FT DOMAIN 82 102
 CC FT TRANSMEM 103 122
 CC FT DOMAIN 123 141
 CC FT TRANSMEM 142 160
 CC FT DOMAIN 161 197
 CC FT TRANSMEM 198 220


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FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 313 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 313 AA; 35523 MW; 6FC174BDC820B3 CRC64;

Query Match 43.5%; Score 704; DB 1; Length 313;
Best Local Similarity 44.8%; Pred. No. 2,1e-47;
Matches 139; Conservative 57; Mismatches 112; Indels 2; Gaps 2;

QY 5 NGNESSATYFIILGIPGLAEQFMAFLPGLCSLYIAVLGNLTIIYVRETHSHHEPMYIF 64
D 5 NDQPHHSSFLGLGIPGLAEQFMAFLPGLCSLYIAVLGNLTIIYVRETHSHHEPMYIF 64
QY 65 LCMISGIDIIISSTSSMPKMLAIFWNSSTIQDPAQLQIPAHISLGSMESTVILMAAFDR 124
D 65 LAMLDSDISLSTATIPKMLGIFWNIKEISFGGYLSQWFFIHFVMSIYLVAAMAFDR 124
QY 125 YVAICHPLEBATVLLPRTVKIGVAAVVGAALMAFLPIKQLEPCRENIISHSYCLHQ 184
D 125 YVACHPLEWTMLISKISLIGAVLKSIVVPLVLLKLPFCGRRIIPHYCEHM 184
QY 185 DVNKLACDDIRVNVVGLIVITISAIGDSLISFSYLLIKTVLGL-TREAQAKAFGTCV 243
D 185 GIARLACASIKVNMIFGL-DSISLLLDVLLILSHIRLIVAVFGLPSWEAKLKALNTG 243
QY 244 SHVCANVFIFVPEIGLSMVRFSKRSDSPVLANTIYLLVPVLPVYGVKTEIROR 303
D 244 SHIGVILAFSTPAFSEFTFHCSDIPQYIHIFLAVLVVPTLPVIVGVRTGIRRT 303
QY 304 ILRLFFVATH 313
D 304 VLRIFKTDH 313

RESULT 11
OXB4_HUMAN STANDARD; PRT; 310 AA.
AC QY5FD;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Olfactory receptor 51b4 (HORS'Detail).
GN OXB4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9228494; PubMed=10220430;
RA Bulger M., van Doornink J.H., Saitoh N., Telling A., Farrell C.M.,
RA Bulger M.A., Feisenfeld G., Axel R., Groudine M.;
RA "Conservation of sequence and structure flanking the mouse and human
beta-globin loci: the beta-globin genes are embedded within an array
of odorant receptor genes."
RT Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134 (1999).
RL [2]
RP ERRATUM.
RA Bulger M., van Doornink J.H., Saitoh N., Telling A., Farrell C.M.,
RA Bulger M.A., Feisenfeld G., Axel R., Groudine M.;
RA Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307 (1999).
RL [3]
RP REVISIONS.
RA MEDLINE=20570519; PubMed=11121057;
RA Bulger M., Bulger M.A., van Doornink J.H., Werten B., Farrell C.M.,
RA Feisenfeld G., Groudine M., Hardison R.;
RA "Comparative structural and functional analysis of the olfactory
receptor genes flanking the human and mouse beta-globin gene
clusters."
RT Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565 (2000).

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CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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-----
DR EMBL; AF137396; AAC29426.2; -
DR Genem; HGNC:14708; OR51B4.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004984; F:olfactory receptor activity; NAS.
DR GO; GO:0007608; P:olfaction; NAS.
DR InterPro; IPR002766; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G-PROTEIN RECP F1; FALSE NEG.
DR PROSITE; PS02624; G-PROTEIN RECP F1; 1.
DR KX MultiGene family; Olfaction.
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 24 47 1 (POTENTIAL).
FT DOMAIN 48 55 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 56 77 2 (POTENTIAL).
FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 99 117 3 (POTENTIAL).
FT DOMAIN 118 136 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 137 155 4 (POTENTIAL).
FT DOMAIN 156 192 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 193 216 5 (POTENTIAL).
FT DOMAIN 217 233 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 234 256 6 (POTENTIAL).
FT DOMAIN 257 271 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 272 291 7 (POTENTIAL).
FT DOMAIN 292 310 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 186 BY SIMILARITY.
FT CARBOHYD 4 4 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 310 AA; 34926 MW; BFE58363BA2EBD67 CRC64;

Query Match 39.1%; Score 632; DB 1; Length 310;
Best Local Similarity 40.5%; Pred. No. 7,4e-42;
Matches 122; Conservative 72; Mismatches 105; Indels 2; Gaps 2;

QY 9 SSATYFIILGIPGLAEQFMAFLPGLCSLYIAVLGNLTIIYVRETHSHHEPMYIF 68
D 5 NSAGPFLITGLGSEAVHAYRISMSFFVITISILFGNLTLLVILMNDLSHEPMYIF 243
QY 69 SGIDIIISSTSSMPKMLAIFWNSSTIQDPAQLQIPAHISLGSMESTVILMAAFDRVAT 128
D 65 ADTDLGWTFTMPVGLVLLDGREIHNAACFQSF-IHSLAVESGILLVLAVDCEIAI 123
QY 129 CHPLRHATVLLPRTVKIGVAAVVGAALMAFLPVLFIKQLEPCRENIISHSYCLHOPVK 188
D 124 RPLRKYCILNSVNMVIGLVLMKGMSTLPIILSYCYPCGSRALLHFPCLHGVIR 183
QY 189 LACDDIRVNVVGLIVITISAIGDSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVC 247
D 184 LACADITFNHIIYPIITQSLTVFDALIIISYLLIKTVNGIASGDEAKSLNVCVSHIS 243
QY 248 AVVFYVPEIGLSMVRFSKRSDSPVLANTIYLLVPVLPVYGVKTEIRORILRL 307
D 244 CVLVFHTVWGLSIRHFGGAPRVAVITMSVYHFLPFPVNVFIISIKTKQIRSLIRL 303
QY 308 F 308
D 304 F 304

RESULT 12

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0252 HUMAN STANDARD; PRT; 319 AA.
 ID 0252 HUMAN STANDARD; PRT; 319 AA.
 AC Q9N0N1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Olfactory receptor 252.
 GN OR252.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 11-319 FROM N.A.
 RA Corby N.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODOANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL, AL135841; CAB96728.1; -.
 DR Genbank; HGNC:8276; OR252.
 DR GO; GO:004984; F:Olfactory receptor activity; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR Multigene family; Olfaction.
 FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 27 50 1 (POTENTIAL).
 FT TRANSMEM 51 58 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 59 80 2 (POTENTIAL).
 FT TRANSMEM 81 101 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 102 121 3 (POTENTIAL).
 FT TRANSMEM 122 140 4 (POTENTIAL).
 FT TRANSMEM 141 159 5 (POTENTIAL).
 FT TRANSMEM 160 196 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 197 220 5 (POTENTIAL).
 FT TRANSMEM 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 238 260 6 (POTENTIAL).
 FT TRANSMEM 261 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 280 299 7 (POTENTIAL).
 FT TRANSMEM 300 319 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 98 190 BY SIMILARITY.
 FT CARBOHYD 5 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 319 AA; 35172 MW; 602602FCA96A179F CRC64;
 Query Match 28.7%; Score 464; DB 1; Length 319;
 Best Local Similarity 35.3%; Pred. No. 6.6e-29;
 Matches 113; Conservative 64; Mismatches 111; Indels 32; Gaps 9;
 QY 7 NSSATY-FILIGL--PELEAQFWLAFPLCSLYLVANGLTIYVTRHSHHEPMY 62
 DB 5 NETSPMGVFLRLSHAPLEKTFVL--ILMLVLVLLGNGVLLTIIDSRHETMY 61
 QY 63 IFCLMISGIDILISTSMKMLAFMNSTTIQFACLLQIFAHISLGMESTVLLMAF 122
 DB 62 FLGNLSFDICFTSSSVPLVDSFLTPQETISFACAVQMLASMACTECLLSMAF 121
 QY 123 DRYVAICHLRAVTLTTPRTYKIGVAA-VRGAAALMAPLVFVKQLPFCNSNIISSYC 181
 DB 122 DRYVAICNPLRYSVIMSKAAVMPMAASSWALGGAASVHTSLAI-QLPFCGDNVINHTPC 180

182 LHODVAKACDDIRVNVVGLIVISAIGLSLISFYLLIKTVGL-TRBAQAKAFG 240
 DB 181 ELIAVLKACADISIVISMEVNTVFLGVPVLFISFVFTITLRLPSAGRKVFS 240
 QY 241 TCYSHVCANFIFVPPPTGLSMVHRESKRDS-----PPLVILNIYLLVPPY 287
 DB 241 TCSAHLTVTVTFYGT--LFFMYGKPKRSDSGADKEDISDKLIFL-----FYGVVTFM 291
 QY 288 LNPVYGVKTRERORILRL 307
 DB 292 LNPITISLRKDVKAARRL 311
 RESULT 13
 ID 015 MOUSE STANDARD; PRT; 312 AA.
 AC P3275;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Olfactory receptor 15 (OR3).
 GN OLFRL5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93028364; PubMed=1384038;
 RA Net P.; Hermans-Borgmeyer I.; Artieres-Pin H.; Beasley L.;
 RA Dione V.E.; Heinemann S.F.;
 RL Spatial pattern of receptor expression in the olfactory epithelium";
 CC Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952 (1992).
 CC -1- FUNCTION: PUTATIVE ODOANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL, M84005; AAA39862.1; -.
 DR FTR; A46247; A46247.
 DR MGD; MGI:106182; Olfrl5.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 DR Multigene family.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 48 1 (POTENTIAL).
 FT TRANSMEM 49 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 79 2 (POTENTIAL).
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 101 120 3 (POTENTIAL).
 FT TRANSMEM 121 139 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 140 160 4 (POTENTIAL).
 FT TRANSMEM 161 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 201 222 5 (POTENTIAL).
 FT TRANSMEM 223 236 6 (POTENTIAL).
 FT TRANSMEM 237 261 7 (POTENTIAL).
 FT TRANSMEM 262 272 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 273 292 7 (POTENTIAL).
 FT TRANSMEM 293 312 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 97 189 BY SIMILARITY.
 FT CARBOHYD 6 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 312 AA; 35172 MW; 602602FCA96A179F CRC64;

SQ SEQUENCE 312 AA; 34333 MW; 8D3877EBB51E132 CRC64;
 Query Match 27.1%; Score 439; DB 1; Length 312;
 Best Local Similarity 34.2%; Pred. No. 5.5e-27;
 Matches 111; Conservative 67; Mismatches 123; Indels 24; Gaps 11;
 CC 2 VDPNGNSSATYFLLIGL---PGLLEAQPWLAFLCSLYLAVALGNLTIIYVREHSH 58
 DB 1 MEVSNSSSGT-FILMGVSDHPHEIFFAV---ILASVLLTVGNLTIIILSRDLARH 56
 QY 59 BPWTFELCMISGDIILLSTSSMPKMLAFWNSTTIOFDCLQIPIAHSLSMESTVLL 118
 DB 57 TPTMFFLSNLSLDAITSSVPMKMLNGPKTISYGGCVQLYVFLWLGATECILLV 116
 QY 119 AMAEDRYVALCHPRLHATVLTLPRTKIGVAAY--VRGALMAPLVPFIKOLPFCRSNLI 176
 DB 117 VMADRYVAVCRPLHYMTVMN-PLIC-WGLAISMVGLGNSVIGSTFTLLQLPFCGRHY 174
 QY 177 SHSICLHODVWKLACDDIRVN--VYGLIYIISAGLSLISFSLIKTVLGL-TRR 233
 DB 175 DNFLCEVPAMIKACGDTSLNEAVLNGVCTFFVVPVSVLV--SYCFIAQAVMKIRSYE 232
 QY 234 AQAFAFCVSHVCAPFIYVPFIQLSMVHRF---SKRSDPLPIVLIANYILVPLNLP 290
 DB 233 GRRAFVTCVSHLVVFLFYG-----SAICYLLPAKSSNOSGKRTISLFSVITPMNP 287
 QY 291 IVYGVKTKRIQRILRLPHVATHAS 315
 DB 288 LITLRNKEVKGALGRLLGKRGAS 312
 RESULT 14
 OLFA_RAT STANDARD; PRT; 312 AA.
 ID OLFA_RAT STANDARD; PRT; 312 AA.
 AC P23273;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Olfactory receptor-like protein 114.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=91191556; PubMed=1840504;
 RA Buck L., Axel R.;
 RT "A novel multigene family may encode odorant receptors: a molecular
 RT basis for odor recognition."
 RL Cell 65:175-187 (1991).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: OLFACTORY BULBEPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL; M64391; AAA41754.1; -
 DR PIR; I23701; I23701.
 DR InterPro; IPR00276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KM G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Multigene family; Olfaction.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT TRANSMEM 80 100
 FT TRANSMEM 101 120
 FT TRANSMEM 121 139
 FT TRANSMEM 140 158
 FT TRANSMEM 159 196
 FT TRANSMEM 197 219
 FT TRANSMEM 220 236
 FT TRANSMEM 237 260
 FT TRANSMEM 261 272
 FT TRANSMEM 273 292
 FT TRANSMEM 293 312
 FT CARBOHYD 5 5
 FT DISULFID 97 189
 SQ SEQUENCE 312 AA; 35718 MW; 08F6546994B1680 CRC64;
 Query Match 26.9%; Score 434.5; DB 1; Length 312;
 Best Local Similarity 33.5%; Pred. No. 1.2e-26;
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;
 QY 7 NESAATYFLLIGLGLLEAQPWLAFLPCLSYLIAVALGNLTIIYVREHSHHEMYTFLC 66
 DB 5 NQTLIEFLGLPSPSHLLPFLATPLAKYLLIIGNLIIYVRLDSHLNPMYPLS 64
 QY 67 MLSGDIILSTSSMPKMLAFWNSTTIOFDCLQIPIAHSLSMESTVLLAADFRRY 126
 DB 65 NLSFSDLCFSSVPMKMLQNNQSQVPSISYGLCTQLYFENVEFDMESFLIVVAAYRYV 124
 QY 127 AICPRLHATVLTLPRTKIGVAAYV-----RAALMAPLVPFIKOLPFCRSNLSHY 180
 DB 125 AICPRLKRTITMS---TKFCASLVLLMLMTHTALHLL-LLARLSFCKNVIIHPF 178
 QY 181 CHQDVWKLACDDIRVN--VYGLIYIISAGLSLISFSLIKTVLGL-TRR 234
 DB 179 CDISALKLCSDIYVNEMLYIIGLIIII-----PFLIVMSYVIFPSILKFPISID 233
 QY 235 QAKAFGCVSHVCAPFIYVPFIQLSMVHRF---SKRSDPLPIVLIANYILVPLNLP 290
 DB 234 IYKVFSTGSHSLVLTLPYGTIFGLYICP--SGNNSVTKETAMAMMYTVVPLNLP 291
 QY 295 VKTKRIQRILRL 307
 DB 292 LNRDMKRALIRV 304
 RESULT 15
 O2C1_HUMAN STANDARD; PRT; 312 AA.
 ID O2C1_HUMAN STANDARD; PRT; 312 AA.
 AC O95371;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 2C1 (Olfm13).
 GN OR2C1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RP MEDLINE=99063798; PubMed=9847080;
 RA Centola M., Chen X., Sood R., Deng Z., Akseutjevich I., Blake T.,
 RA Riecke D., Chen X., Wood G., Zaks N., Richards N., Krizman D.,
 RA Mansfield E., Apostolou S., Liu J., Shafran N., Vedula A., Hamon M.,
 RA Cercek A., Kahan T., Gumucio D., Callen D.F., Richards R.I.,
 RA Moyzis R.K., Doggett N.A., Collins F.S., Liu P.P.,
 RA Fischer-Chodasian N., Kastner D.L., 700 kb transcript map around the
 RT Construction of an approximately 700 kb transcript map around the
 RT familial Mediterranean fever locus on human chromosome 16p13.3."
 RL Genome Res. 9:1-21 (1998).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO: FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF098664; AAC83557.1; -.
DR Genbank; HGNC:8242; ORC1.
DR GO; GO:0004984; F:olfactory receptor activity; TAS.
DR InterPro; IPR002076; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25
FT TRANSSEM 26 49
FT DOMAIN 50 57
FT TRANSSEM 58 79
FT DOMAIN 80 100
FT TRANSSEM 101 120
FT DOMAIN 121 139
FT TRANSSEM 140 158
FT DOMAIN 159 196
FT TRANSSEM 197 216
FT DOMAIN 220 236
FT TRANSSEM 237 259
FT DOMAIN 260 272
FT TRANSSEM 273 292
FT DOMAIN 293 312
FT DISULFID 97 189
FT CARBOHYD 5
SQ SEQUENCE 312 AA; 34506 MW; CC40D7D349BEBB9E7 CRC64;
Query Match 26.7%; Score 432.5; DB 1; Length 312;
Best Local Similarity 35.4%; Pred. No. 1.7e-26;
Matches 102; Conservative 58; Mismatches 136; Indels 9; Gaps 5;
QY 7 NESATATFTIIGLPGLEAEQFWLAFPLCSLTILAVLGNLTITIVRTSHLHEPMYFLC 66
Db 5 NDSLSLGQFVLMSSIDHPQLQEMIFIALFTSVLLTLNLSSTIILSRLEAHLHFMVFLS 64
QY 67 MLSSGIDILISTSSSPKXLAIFWENSTTIQDPACILQIFALHLSGSESTVLLAMAFDRYV 126
Db 65 NLSLDIAFAFTSSPQMLINLMGDKTISYGGCTTCITQVVELMGATGCILLVNAFDRYV 124
QY 127 AICGPHLHATVLTLPRTKIGVAIVVGAALMALEPLFIKQLPFCRSNLSISYCLHODV 166
Db 125 AVCRPLAFATNIMNPQLCMILAVIAMGGLGNSVIGSFITQLPLCGHRRVVGFLCEVPAM 164
QY 187 MKLACDDIRVN--VYGLIYIISAIGDSLISISYLLIKTVIGL-TREDAQKAFGTCV 243
Db 185 IKACGGTISNQAAVLNVCTFFTAVPISITVI--SYCLIAQAVLKIKHSAGRRRAFTCL 242
QY 244 SHVCAVFIY-VPTIGLSMWHRFKSRDSPLEVIANIYLLVPLVNLPIVYGVTKEIRQ 302
Db 243 SHLLVIVFLFGSASVGYLLPAKSKSQDQGK---FISLFGLVNPMVNPFLITYLRNWEYKG 299
QY 303 RIIRLL 307
Db 300 ALIRLL 304

```

Search completed: February 9, 2004, 16:24:16
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 16:22:06 / Search time 20 Seconds
(without alignments)
1524.274 Million cell updates/sec

Title: US-10-017-066a-2

Sequence: 1 MVDPMNGESSATYFLILGHP.....KEIRQRILRLPVTATHASEP 317

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 76: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	552	34.1	292	2 A60547	hypothetical prote
2	473.5	29.3	313	2 E45774	odorant receptor 8
3	453	28.0	307	2 S29710	olfactory receptor
4	439	27.1	312	2 A46247	olfactory receptor
5	434.5	26.9	312	2 I23701	olfactory receptor
6	431.5	26.7	310	2 E23701	olfactory receptor
7	430.5	26.6	319	2 JCS624	olfactory receptor
8	429.5	26.6	312	2 S29708	olfactory receptor
9	428	26.5	328	2 G45774	odorant receptor 2
10	427.5	26.4	314	2 S20572	olfactory receptor
11	423.5	26.3	314	2 A37286	olfactory receptor
12	423.5	26.2	314	2 S29707	olfactory receptor
13	420.5	26.0	321	2 H45774	odorant receptor 3
14	418.5	25.9	305	2 S29711	olfactory factor 0
15	418.5	25.9	309	1 S51356	olfactory receptor
16	413	25.5	312	2 A48413	probable olfactory
17	411	25.4	160	2 S58066	probable olfactory
18	411	25.4	160	2 S58066	probable olfactory
19	407.5	25.2	311	2 I45774	odorant receptor 1
20	407	25.2	313	2 S20571	chemoreceptor TB33
21	404.5	25.0	312	2 G23701	olfactory receptor
22	404.5	25.0	313	2 B23701	olfactory receptor
23	402.5	24.9	311	2 C23701	olfactory receptor
24	402.5	24.9	314	2 H23701	olfactory receptor
25	401	24.8	317	2 F45774	odorant receptor 4
26	396.5	24.5	316	2 A57069	olfactory receptor
27	395.5	24.5	328	2 A45774	odorant receptor 3
28	395.5	24.5	328	2 A45774	odorant receptor 3
29	393.5	24.3	328	2 B45774	odorant receptor 3

30	390.5	24.1	320	2 S20573	olfactory receptor
31	388.5	24.0	312	2 A46750	olfactory receptor
32	386.5	23.9	304	2 S29709	olfactory receptor
33	384.5	23.8	315	2 UC5836	olfactory receptor
34	383.5	23.7	328	2 C45774	odorant receptor 3
35	383	23.7	333	2 A23701	olfactory receptor
36	379.5	23.5	327	2 F23701	olfactory receptor
37	375	23.2	317	2 D23701	olfactory receptor
38	370	22.9	315	2 JC5201	chemoreceptor TB56
39	368.5	22.8	315	2 JC4658	olfactory receptor
40	366	22.6	318	2 JC5202	chemoreceptor TB64
41	313.5	19.4	234	2 S29000	G protein-coupled
42	310.5	19.2	222	2 B40745	odorant receptor (
43	303.5	18.8	264	2 PC4369	olfactory receptor
44	289.5	17.9	234	2 S28999	G protein-coupled
45	285.5	17.7	222	2 D40745	odorant receptor (

ALIGNMENTS

RESULT 1

A60547 hypothetical protein (HPRH breakpoint 3' region) - human (fragment)

N/Alternate names: olfactory receptor homolog

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 26-Aug-1999

C/Accession: A60547; A60482

R/Feingold, E.A.; Forget, B.G.

Blood 74, 2178-2186, 1989

A/Title: The breakpoint of a large deletion causing hereditary persistence of fetal hemo

A/Reference number: A60547; PMID:90028751; PMID:2478223

A/Accession: A60547

A/Molecule type: DNA

A/Residues: 1-292 <FEI>

C/Superfamily: olfactory receptor OR14

Query Match 34.1%; Score 552; DB 2; Length 292;

Best Local Similarity 40.3%; Pred. No. 2.2e-41;

Matches 114; Conservative 49; Mismatches 88; Indels 32; Gaps 6;

Qy	16	LIGPGLEAQAQFWLAPLGLVLAVALGNTIIVYRTSHLHPYFLMGIDILI	75
Db	29	LVGPGLESVQCWIGPFCALYILAMIGNSLITKSRSLHPYIFLGMGARDIAL	88
Qy	76	STSGMPKMLAIFPNSTTIOFDCLOIF-----AIH-SLSGMESTVLLAMFDSYVAI	128
Db	89	ASSIMPRMGLGSGL-----WCLKSLIPACENVVHPHIGIESGILVAMALDRYVAI	140
Qy	129	CHPLRHATVTLTPRVTKIGVAAYVGAALMAPLPVEIK-OLPFCRANILSHSYCLHQDVW	187
Db	141	CYPLRHANITFHLQVIGTMVYLRALILVAPCHVLIKRFQYHTTVISHSYCEMAIIV	200
Qy	188	KIACDDIRNVVYGLVYISATIGDSILTSFVILLKTYLGL-TBEAQAKAGTCVSHV	246
Db	201	KLAANVQVKKIKIGLFAVFAAGFDLFTLSYIQFIVFRLPQGEARKAENTCIAMT	260
Qy	247	CAVIFVYVPFVIGLVMHREKRDSPVLINIVLVPPVLN	289
Db	261	CVLQLFYLLAFPSFFTHRFSSH-----IPFYIH	288

RESULT 2

E45774 odorant receptor 8 - channel catfish

C/Species: Ictalurus punctatus (channel catfish)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 26-Aug-1999

C/Accession: E45774

R/Neel, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A/Title: The family of genes encoding odorant receptors in the channel catfish.

A/Reference number: A45774; PMID:93201590; PMID:7916654

A/Accession: E45774

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 12313 <NG>

A:Experimental source: olfactory epithelium

A>Note: sequence extracted from NCBI backbone (NCBI:127748)

C:Superfamily: olfactory receptor OR14

C:Keywords: olfaction; transmembrane protein

Query Match 29.3%; Score 473.5; DB 2; Length 313;

Best Local Similarity 34.1%; Pred. No. 2.1e-34;

Matches 105; Conservative 66; Mismatches 132; Indels 5; Gaps 4;

QY 1 WVDNGNESSATYFILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSHHP 60
DB 1 MIAPONISFTT-FLUTGFHDGEGPILSIPYLLMFLSTSLTIIYILISGRALHSP 59
QY 61 MYIFLCMSGIDILISTSSMPKMLAFWFNSTTIQPDACLOIPAHISLGSMESTVLLM 120
DB 60 MCILGLMAVVDLSMPICVPMMLISFLFNKGISLVGLVQWQCHCAGTFOSTILLMM 119
QY 121 AEDRYVAICHPLRHATVLTLPRTVKIGVAAVRGAALMAPLPVFIKQLPFCRSNLSHSY 180
DB 120 ALDREFAICRPLPYQKXWGMENPLKFIIFPIRMLPFTTIVSAGKLTFCENIDHCY 179
QY 181 CLHQVMKLACDDIRVNVVGLIVISAIGDSLISFSTYLLIKTVGLTREQAQAFG 240
DB 180 CEHMAVYOLACGDISINNALGLTVFPLTTADPFITISYVILVISTL-RSGKACIKAVN 238
QY 241 TCVSHVCAVFIYVYFPIGLSMWHRFSKRSDPLP-VIIANIYLLVPVLPVIVGVTKY 299
DB 239 TCIHTIIMTVSLNPLALIAFISYRI--RNFSPSRVLSMTMYLFIPOCRPIIIVGVTKY 296
QY 300 IRQRIKL 307
DB 297 IREQFLK 304

RESULT 3

olfactory receptor OR18 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998

C:Accession: S29710

R:Ramberg, K.; Krueger, J.; Strommann, J.; Boekhoff, I.; Kubick, S.; Baumstarck, C.; Breez

Nature 361, 353-356, 1993

A>Title: Cloning and expression of odorant receptors.

A:Reference number: S29707; MUID:93149273; PMID:7678922

A:Accession: S29710

A:Molecule type: mRNA

A:Residues: 1-307 <RAM>

C:Superfamily: olfactory receptor OR14

Query Match 28.0%; Score 453; DB 2; Length 307;

Best Local Similarity 33.6%; Pred. No. 1.4e-32;

Matches 107; Conservative 64; Mismatches 125; Indels 22; Gaps 7;

QY 6 GNESSATYFILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSHHP 62
DB 2 GENNNITRIFILGLTOPDGRKALFVIF--LIYITMGNLLIIVTVIASLSLSPMY 56
QY 63 IFELCMISGIDILISTSSMPKMLAFWFNSTTIQPDACLOIPAHISLGSMESTVLLM 122
DB 59 FFLASLSLIDLFTFAISPKLIADLDOKTISRACMSQLFEHFGVDIVILVAMAY 118
QY 123 DRYVAICHPLRHATVLTLPRTVKIGVAAVRGAALMAPLPVFIKQLPFCRSNLSHSY 182
DB 119 DRYVAICHPLRHATVLTLPRTVKIGVAAVRGAALMAPLPVFIKQLPFCRSNLSHSY 178
QY 183 HQDVMKLACDDIRVNVVGLIV--ISAIGDSLISFSTYLLIKTVGLTREQAQAFG 238
DB 179 MSPLLVACDD--TYPIGLTVIANGVNCIVIFTLGLG-SYGIIRLSLTQSQEGRRA 234
QY 239 FGTCVSHVCAVFIYVYF--FIGLSMWHRFSKRSDPLP-VIIANIYLLVPVLPVIVGVTKY 296

DB 235 LSTGSHLIVLTFVFPFCIMFARPVNF-----PIDKCTVFETITPMPLNPLIYTLR 288

QY 297 TREIRORILRPHVATHA 314

DB 289 NSEIKCMKMLCKMFLA 306

RESULT 4

A:Accession: A46247

olfactory receptor OR3 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A46247

R:Ref. P.; Hermans-Borgmeyer, I.; Artberg-Pin, H.; Beasley, L.; Dione, V.E.; Heinemann

Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992

A>Title: Spatial pattern of receptor expression in the olfactory epithelium.

A:Reference number: A46247; MUID:93028384; PMID:1384038

A:Accession: A46247

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-312 <NEP>

A:Cross-references: GB:M4005; NID:g200153; PIDN:AAA39662.1; PID:g200154

A>Note: sequence extracted from NCBI backbone (NCBI:115362)

C:Superfamily: olfactory receptor OR14

Query Match 27.1%; Score 439; DB 2; Length 312;

Best Local Similarity 34.2%; Pred. No. 2.4e-31;

Matches 111; Conservative 67; Mismatches 123; Indels 24; Gaps 11;

QY 2 VDPNGNESSATYFILIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSHHP 58
DB 1 MEVDNSSSGT-FILMGVSDHPLHLEIFFAV---ILASYLLTLVGNLTIIILSRDLALH 56
QY 59 EPMYIFLCMSGIDILISTSSMPKMLAFWFNSTTIQPDACLOIPAHISLGSMESTVLL 118
DB 57 TMYIFFLNLSLDAFTTSVPQMLKMLNGPDKTISGCVTQLYVPLMGATRECLIV 116
QY 119 AMAEDRYVAICHPLRHATVLTLPRTVKIGVAAV--VRGAALMAPLPVFIKQLPFCRSNLT 176
DB 117 VMAEDRYVAICHPLRHATVLTLPRTVKIGVAAV--VRGAALMAPLPVFIKQLPFCRSNLT 174
QY 177 SHSYCLHODWKLACDDIRVNVVGLIVISAIGDSLISFSTYLLIKTVGLTRE 233
DB 175 DNFLCEVAMIKLACGDISLNEAVANGVCTFTVVPVSVILV--SYCIAQAVMKIRSV 232
QY 234 AQAKAFGTGVSHVCAVFIYVYFPIGLSMWHRF---SKRRDSPLPVILANIYLLVPVLP 290
DB 233 GRRKAFNTGVSHLVVVFIFYG---SALYGYLLPAKSSNQSQKFTSLFYSVVTPMVNP 287
QY 291 IYGVYKTEIKRILRPHVATHA 315
DB 288 LYTTRKNEVAGALGRILGKGRGAS 312

RESULT 5

olfactory receptor OR14 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999

C:Accession: 123701

R:Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A>Title: A novel multigene family may encode odorant receptors: a molecular basis for ol

A:Reference number: A23701; MUID:91191556; PMID:1840504

A:Accession: 123701

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-312 <BUC>

A:Cross-references: GB:M4391; NID:g205843; PIDN:AAA41754.1; PID:g205844

C:Superfamily: olfactory receptor OR14

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	26.9%;	Score 434.5;	DB 2;	Length 312;
Best Local Similarity	33.5%;	Pred. No. 6e-31;		
Matches 105;	Conservative 64;	Mismatches 119;	Indels 25;	Gaps 7

```

QY 7 NESATAEIILIGLEGEAEQEWLAFPLCSYLLIWLNLNTIIVVREHSHHEMZYFLC 66
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 5 NQTLIEFLILGLIIPSEYHLLFYALFLAWYLTIIILGNLIIVLRDSHLHMPYIFLS 64
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 67 MLGSDILILISTSMPKLALFWMNSTTIQPDACLQIFALHLSGMSYVLLAMAFRIV 126
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 65 NLSSSDICFSSVTPMKLQNMQSOVPSISYGCITCQYFEWFGDMSSFLLVWAXYRYV 124
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 127 AICPELRATVLTTPRVTKIGVAAV-----RGAAALAPLPVRIKOLPCRSNLSHSY 180
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 125 AICPELRATTIMS-----TKFCASLVLLMLTMTHALLHTL--LIARLSFCOKVILAHFF 178
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 181 CLHQDWMLACDDIRVN-----VYGGIIVISALGDSLISFYLLIKTVGL--IREA 234
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 179 CDISALELCSDIYVVELMITYIIGSLITII-----PFLIVMSYVIRFSLILFSPSIQD 233
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 235 QAKAFGTCVSHVCAVFIYPVPIGLSMVHRESKRDSPLPYLITANIYLLVPVLPNPIYVG 294
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 234 IYKVFSTGSHLSVYTLFYGTIFGIYLCR--SGNNSFWKEIAMAMMYTVVTPMLNPFIYS 291
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 295 VKTKEIRQRIURL 307
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 292 LRANDMKALIRV 304
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

RESULT 6

Olfactory receptor 13 - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
C|Accession: E23701
R|Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A|Title: A novel multigene family may encode odorant receptors: a molecular basis for coo
A|Reference number: A23701, MUID:91191556, PMID:1840504
A|Accession: E23701
A|Status: nucleic acid sequence not shown
A|Molecule type: mRNA
A|Residues: 1-310 <BUC>
A|Cross-references: GB:M64385; NID:g205831; PIDN:AAA1748.1; PID:g205832
C|Superfamily: olfactory receptor OR14
C|Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match      26.7%;  Score 431.5;  DB 2;  Length 310;
Best Local Similarity 33.2%;  Pred. No. 1.1e-30;
Matches 102;  Conservative 71;  Mismatches 121;  Indels 13;  Gaps 7;

QY      NESAATYIIILGLPELEBAQ--FWLAFLPLCLYLIVANGNLTITTYIVRTHESLSHEPYIF 64
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
Db      3  NOTFTTQPLLLGLPFBESHQHLFYALFLV--MYLTTIIGNLTIIIVLVQDSQLTWMLF 60
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
QY      65  LCMLSGDIILISTSSMPMLAIWFENSTTIOFDACLOIFAHSLSGSESTVLLAMAFDR 124
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
Db      61  LSNLSFSDLCSSVYMKPLQNMRSQDTSIPGCGLAQTFPMVPGDMESFLVAMAYDR 120
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
QY      125  YVATHEPVRHATVTLTPRYTKIGVA--AVVRGAALMAPLVFIKQLPFCGNSNIISSYC 181
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
Db      121  YVALCFPLHTYSIMS-FYKCTCLVLLMWLTTSHMAWTL--LAARLSFCERNVVLNFFC 177
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
QY      182  LHQDVTKACDDIRVNVVYGLVIVISAIGLDSLISFSYLIILKVLGL-TREAOAKAFG 240
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
Db      178  DLFLVTLKLCASCTTYNEENMIFMSTLLIIIPPELLVMSYARISSILKVPSTGICAKFS 237
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
QY      241  TCVSHVCAVFIFYPVFIGLSMYHRSKRDSPLPYILANIIYLLVPVLPVPIYGVYKTEI 300
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
Db      238  TCGSHLSVSLVLEYGIIIGLYLCP--AGNNSTYKEMVMAMMTVTVPMLNPFYISLRNDM 295
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:
QY      301  RQRIIRL 307
      :.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:.:

```

Db 296 KRALIV 30

RESULT 7

Olfactory receptor HTRCR92 - human
 C|Species: Homo sapiens (man)
 C|Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
 C|Accession: JCS624; S58003
 R|Vanderheeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 A|Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed
 A|Reference number: JCS624; MIMD:97415789; PMID:5268701
 A|Contents: Testis
 A|Accession: JCS624
 A|Molecule type: mRNA
 A|Residues: 1-319 <VAM>
 A|Cross-references: GB|Y10530; NID:G2792017; PIDN:CAA71558.1; PID:G2792018
 R|Vanderheeghen, P.; Schumann, S.; Vassart, G.; Parmentier, M.
 A|Submitted to the EMBL Data Library, July 1995
 A|Description: Male germ cells from several mammalian species express a specific repertoire
 A|Reference number: S57995
 A|Accession: S58003
 A|Molecule type: mRNA
 A|Residues: 126-282 <VAM>
 A|Cross-references: EMBL:X89677; NID:G902337; PIDN:CAA61824.1; PID:G902338
 C|Genetics:
 A|Map position: 19p13.1
 C|Function:
 A|Description: Involved in control of sperm physiology
 C|Superfamily: Olfactory receptor OR14
 C|Keywords: G protein-coupled receptor; transmembrane protein
 F|26-48/Domain: transmembrane #status predicted <TM1>
 F|58-79/Domain: transmembrane #status predicted <TM2>
 F|101-120/Domain: transmembrane #status predicted <TM3>
 F|140-164/Domain: transmembrane #status predicted <TM4>
 F|197-218/Domain: transmembrane #status predicted <TM5>
 F|237-260/Domain: transmembrane #status predicted <TM6>
 F|272-292/Domain: transmembrane #status predicted <TM7>

	Query Match	26.6%;	Score 430.5;	DB 2;	Length 319;
	Best Local Similarity	33.3%;	Pred. No. 1.4e-30;		
	Matches 102;	Conservative 71;	Mismatches 118;	Indels 15;	Gaps 8;
OY	6	GNESATYFLLIL---	PGLEBAQFWLAPPCSLYVIAVIGNLTIIYIVRTEHSLHEPMY	62	
OY	7				
Db	4	GNTQISEFLLFSGEPGLQPFPLGL---	FLSMVTVLGNLIIILATISDSHLEHTPMY	60	
OY	63	IFPCMLSGDILISTSGMPMLAIFWNSNTTIOFDACLLQIPAIHLSGMSERVLLAMP	122		
OY	61	FFISNISEFAI	CYTSTTIPMIMNIOTQNKVLTIVYACLMQMFPIIPAGENFLISVMAI	120	
OY	123	DRVVAICHPLEHATVTLPRVTKIGVAAVVRGAALMAPPV-FIKOLPFCRSNIIISHSYC	181		
Db	121	DRFAIACHPL-HYVMVNNPHLCGLIVLASWTMSALYSLQILMVVRLSPFTALEIHPFC	179		
OY	182	LHQDVMKACDDLRNV--VYEGIVITISAGDLSLISFSYLLILKTVLGL-TREAQATA	238		
Db	180	ELNVQIOLASDSFELHMVIYFTVALLGGGPLGLL--YSKSIISIHAISSAQKYKA	237		
OY	239	FGICVSHVCAVFIFYYPFGLSMVHRFSKRKDEPLVILANTIVLPPVLPVPGVVKR	298		
OY	238	FSTASHLSVSLFYALIGVYL--SSAATRNHSHSATAISVMYTVLPMLNPITISLRNK	295		
OY	299	EIRORI	304		
OY					
Db	296	DIKAL	301		

RESULT

olfactory receptor OR12 - rat
C;Species: Rattus norvegicus (Norway rat)

C/Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C/Accession: S29708
 R/Ranking: K.; Krieger, J.; Strochmann, J.; Boehkoff, I.; Kubick, S.; Baumstark, C.; Breez
 Nature 361, 353-356, 1993
 A/Title: Cloning and expression of odorant receptors.
 A/Reference number: S29707; MUID:93149273; PMID:7676922
 A/Accession: S29708
 A/Molecule type: mRNA
 A/Residues: 1-312 <RAM>
 C/Superfamily: olfactory receptor OR14

Query Match 26.6%; Score 429.5; DB 2; Length 312;
 Best Local Similarity 31.7%; Pred. No. 1.7e-30;
 Matches 98; Conservative 75; Mismatches 119; Indels 17; Gaps 6;

QY 7 NESASATYFLIGPGLEAQLAF--PLCSLYLAVNGNTIIVTETHSHPEWIF 64
 DB 5 NQTVISQFLILGLP--IPPEHMLFTYLLAMYLITLIGNLITLILDSLHIMYLF 62
 QY 65 LCMLESGIDILISTSSMPKMLAFWNSITIQDACLQIFAIHSLSGNESTVLLAMAFDR 124
 DB 63 LKSLSPSDICFSSVMPKILQNMNQDSTITYTGLTQWFSMPAGMEIFLVSMAYDR 122
 QY 125 YVAICPLRHATVLTLPRTKIGVAAVVGALMAPLPVFIKQLPFGCSNLSHSYCLHQ 184
 DB 123 YVAICPLRHATVLTLPRTKIGVAAVVGALMAPLPVFIKQLPFGCSNLSHSYCLHQ 182
 QY 185 DWKLACDDIRVN----VYGLIVISAIGLSLISFSYLLIKTVGL-TREAQAKA 238
 DB 183 ALTKACSDTYINEMIFLIGLTVI----PFLIIVTWYQVICSILTKPSRAIKI 237
 QY 239 FGTGVSHVCAVFIFFYVPIFGLSMVRHSKRDSPLPYLIANIYLLVPVLANPIYGVKTK 298
 DB 238 FSTCGSHLSTVSLFYGTVIGLYLC--SSANSTVKEVWAMMIVTVMNPFIYSILNR 295
 QY 299 EIRQIRLRL 307
 DB 296 DIKELALVRV 304

RESULT 9
 G45774
 odorant receptor 202 - channel catfish
 C/Species: Ictalurus punctatus (channel catfish)
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998
 C/Accession: G45774
 R/Ranking: U.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.
 Cell 72, 657-666, 1993
 A/Title: The family of genes encoding odorant receptors in the channel catfish.
 A/Reference number: A45774; MUID:93201590; PMID:7916654
 A/Accession: G45774
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-328 <NGA>
 A/Experimental source: olfactory epithelium
 A/Note: sequence extracted from NCBI backbone (NCBIP:127746)
 C/Superfamily: olfactory receptor OR14
 C/Keywords: olfaction; transmembrane protein

Query Match 26.5%; Score 428; DB 2; Length 328;
 Best Local Similarity 29.4%; Pred. No. 2.4e-30;
 Matches 92; Conservative 76; Mismatches 127; Indels 18; Gaps 7;

QY 4 PNGNESSATYFLIGPGLEAQLAF--APPLCSLYLAVNGNTIIVTETHSHPEWIF 62
 DB 2 PEGNINNVKXVFLIGPGLPBNVYGLVSMFVYVCTLIGNCTPFLFLRKSILQKMY 61
 QY 63 IFCKMSGDILISTSSMPKMLAFWNSITIQDACLQIFAIHSLSGNESTVLLAMAF 122
 DB 62 YMLNLNLAASDVLESTLTPKILARVFGSGISFPGCFIQKQFVHPATVNLAVLAWAF 121
 QY 123 DRYVAICPLRHATVLTLPRTKIGVAAVVGALMAPLPVFIKQLPFGCSNLSHSYCL 182

DB 122 DRYVAICNPLRVNIVKESTIILGLCVVSWLBAEPVLTTVIRATSLPYCASNTVILQYCD 181
 QY 183 HQDVKLACDDIRVNVVGLIVISAIGL---DSLISFSYLLIKTVGL-TREAQAKA 238
 DB 182 HVSVTKLACID--RRPYAFPLVSAVLMPLPLFIIFSYSIIVTERTSTGRKTK 238
 QY 239 FGTGVSHVCAVFIFFYV---FIGLSM-VHRFSKRDSPLPYLIANIYLLVPVLANPIY 293
 DB 239 LSTCSSQLIITITFLPRLCLNLTSSLSGIH-----INADIQILVMYLSLPLPMNPVY 293
 QY 294 GVKTKAIRQIRLR 306
 DB 294 CLRTKRAKEKELKR 306

RESULT 10
 S20572
 olfactory receptor - human
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
 C/Accession: S20572
 R/Ranking: M.; Libert, F.; Schumann, S.; Schifmann, S.; LeFort, A.; Eggerickx, D.;
 Nature 355, 453-455, 1992
 A/Title: Expression of members of the putative olfactory receptor gene family in mamma
 A/Reference number: S20571; MUID:92131132; PMID:1370859
 A/Accession: S20572
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-314 <PAR>
 A/Cross-references: EMBL:X64994; NID:932085; PID:CAA46127.1; PID:932086
 C/Superfamily: olfactory receptor OR14
 C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.4%; Score 427.5; DB 2; Length 314;
 Best Local Similarity 34.5%; Pred. No. 2.5e-30;
 Matches 108; Conservative 64; Mismatches 120; Indels 21; Gaps 8;

QY 7 NESASATYFLIGPGLEAQLAF--PLCSLYLAVNGNTIIVTETHSHPEWIFLC 66
 DB 5 NQTVISQFLILGLP--IPPEHMLFTYLLAMYLITLIGNLITLILDSLHIMYLF 62
 QY 67 LMSGIDILISTSSMPKMLAFWNSITIQDACLQIFAIHSLSGNESTVLLAMAFDRVY 126
 DB 65 NLSFSDICFSSVTPKILQNMNQDPSIPVADCLTQWFSMPAGMEIFLVSMAYDRVY 124
 QY 127 YVAICPLRHATVLTLPRTKIGVAAVVGALMAPLPVFIKQLPFGCSNLSHSYCLHQ 183
 DB 125 YVAICPLRHATVLTLPRTKIGVAAVVGALMAPLPVFIKQLPFGCSNLSHSYCLHQ 181
 QY 184 QDVKLACDDIRVN----VYGLIVISAIGLSLISFSYLLIKTVGL-TREAQAK 237
 DB 182 SALKLKAFSDTRNEMVIFIMGLIIVT---PFLIIGSVARIYSILTKVSSKIGCK 236
 QY 238 AFGTCVSHVCAVFIFFYVPIFGLSMVRHSKRDSPLPYLIANIYLLVPVLANPIYGVK 296
 DB 237 AFGTCGSHLSVSLFYGTVIGLYLC--SSANSTLKTQVWAMMIVTVMNPFIYSILNR 293
 QY 297 TKRIRQIRLRF 309
 DB 294 NRDMAKALSRVH 306

RESULT 11
 A37286
 olfactory receptor 115 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-Aug-1999
 C/Accession: A37286
 R/Ranking: L.; Axel, R.
 Cell 65, 175-187, 1991
 A/Title: A novel multigene family may encode odorant receptors: a molecular basis for od
 A/Reference number: A23701; MUID:91191556; PMID:1840504
 A/Accession: A37286

A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-314 <BUC>
 C:Cross-references: GB:M64392; NID:9205845; PID:AAA41755.1; PID:9205846
 C:Superfamily: olfactory receptor OR14
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.3%; Score 425.5; DB 2; Length 314;
 Best Local Similarity 33.2%; Pred. No. 3.8e-30;

Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;

QY 7 NESATYFLIGLPGLEAQQ--FWLAPLCSLYLAVIGNLTIYIVTSHSLHEPMYIF 64
 DB 5 NOTVISOFLILFLPPESEHGVYALF--LSKYLTVTIGNLIIILILHDSHLHTPMYLF 62
 QY 65 LCMISGIDILISTSSMPKMLAFWENSTTIQFDACLIQIFAHISLGSVESTVLLAMAFDR 124
 DB 63 LSNLSPSDLCFSSVMPKLLQNMOSQVPSIPAGCLTQLYFYLYPADESLFLVAMAYDR 122
 QY 125 YVAICHPLRHATVLTLPRTKIGVAAYVGAALM---APL-PVFIKQLPFGCSNLSHSY 180
 DB 123 YVAICHPLRHATVLTLPRTKIGVAAYVGAALM---APL-PVFIKQLPFGCSNLSHSY 178
 QY 181 CLHODVMKACDDIRNVVYGLVITISALGDSLLISFSYLLIKTLVGL-TREA 234
 DB 179 CDISPLKLSGSDTHNNEVLIVMGSLVIVIPFV---LIIVSARVVASILKVPSSRG 233
 QY 235 QAKARCTCHVCAVFIYVFPFGISWVHRFSKRDSPLVILANTYLLVPPVNPVYVG 294
 DB 234 HKISTCSHLSVSLFYGLIIGLYLCP--SANNSTVKEVMMMYTVVPMNPFYIS 291
 QY 295 VTKKEIRRIRL 307
 DB 292 LNRDMKEALIRV 304

RESULT 12

S29707

olfactory receptor OR5 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999

C:Accession: S29707; B37286

R:Ramung, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer

Nature 361, 353-356, 1999

A>Title: Cloning and expression of odorant receptors.

A:Reference number: S29707; PMID:93149273; PMID:7678922

A:Accession: S29707

A:Molecule type: mRNA

A:Residues: 1-314 <RAM>

R:Buck, L.; Axel, R.

Cell 65, 175-187, 1991

A>Title: A novel multigene family may encode odorant receptors: a molecular basis for od

A:Reference number: A23701; PMID:91191556; PMID:1840504

A:Accession: B37286

A:Molecule type: mRNA

A:Residues: 193-236 <BUC>

A:Cross-references: GB:M64375; NID:9205811; PID:AAA41738.1; PID:9205812

C:Superfamily: olfactory receptor OR14

C:Keywords: G protein-coupled receptor; membrane protein

Query Match 26.2%; Score 423.5; DB 2; Length 314;
 Best Local Similarity 34.4%; Pred. No. 5.7e-30;

Matches 104; Conservative 64; Mismatches 119; Indels 15; Gaps 7;

QY 7 NESATYFLIGLPGLEAQQ--FWLAPLCSLYLAVIGNLTIYIVTSHSLHEPMYIF 64
 DB 5 NOTVISOFLILFLPPESEHGVYALF--LSKYLTVTIGNLIIILILHDSHLHTPMYLF 62
 QY 65 LCMISGIDILISTSSMPKMLAFWENSTTIQFDACLIQIFAHISLGSVESTVLLAMAFDR 124
 DB 63 LSNLSPSDLCFSSVMPKLLQNMOSQVPSIPAGCLTQLYFYLYPADESLFLVAMAYDR 122

QY 125 YVAICHPLRHATVLTLPRTKIGVAAYVGAALM---APL-PVFIKQLPFGCSNLSHSY 180
 DB 123 YVAICHPLRHATVLTLPRTKIGVAAYVGAALM---APL-PVFIKQLPFGCSNLSHSY 178
 QY 181 CLHODVMKACDDIRNVVYGLVITISALGDSLLISFSYLLIKTLVGL-TREAQAKF 239
 DB 179 CDMALKKACSDTRNEVVFIVSLFVLPALTIMSVRIVSLKVPSSQGIYKAF 238
 QY 240 GTCVSHVCAVFIYVFPFGISWVHRFSKRDSPLVILANTYLLVPPVNPVYGVYKKE 299
 DB 239 SSCGSHLSVSLFYGVIVLYLCP--SSNNSTVKEVMMMYTVVPMNPFYISLRND 296
 QY 300 IR 301
 DB 297 IR 298

RESULT 13

H45774

odorant receptor 3 - channel catfish

C:Species: Ictalurus punctatus (channel catfish)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998

C:Accession: H45774

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A>Title: The family of genes encoding odorant receptors in the channel catfish.

A:Reference number: H45774; PMID:93201590; PMID:7516654

A:Accession: H45774

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-321 <NGA>

A:Experimental source: olfactory epithelium

A:Note: sequence extracted from NCBI backbone (NCBI:127745)

C:Superfamily: olfactory receptor OR14

C:Keywords: olfaction; transmembrane protein

Query Match 26.0%; Score 420.5; DB 2; Length 321;
 Best Local Similarity 32.4%; Pred. No. 1.1e-29;

Matches 101; Conservative 69; Mismatches 127; Indels 15; Gaps 6;

QY 9 SSMATY-----FLIGLPGLEAQQFWLAPLCSLYLAVIGNLTIYIVTSHSLHEPMYIF 63
 DB 14 TMTFIRPSTFYITGLYNIIPKAYYLF-LCPVYVTVTFGNSFIMGITILARSLTAKYI 72
 QY 64 FLCLMSGIDILISTSSMPKMLAFWENSTTIQFDACLIQIFAHISLGSVESTVLLAMAFDR 123
 DB 73 AYFNALASDLCSSALIPKLDMLFENOSIYERACLSMFFVYCMITLQCTLLALAYD 132
 QY 124 RYVAICHPLRHATVLTLPRTKIGVAAYVGAALM---APL-PVFIKQLPFGCSNLSHSY 183
 DB 133 RLTAICPYRHAIVKAMIFILGAMVLSVAVNALVALITRISFCSTTVYSYFCDH 192
 QY 184 QDVMKACDDIRNVVYGLVITISALGDSLLISFSYLLI---LKTVGLTREQAQAKF 239
 DB 193 GRVYKACDNTNINSMGVCATILYFLILISYVIGALGXKLAGV---EYVKAM 249
 QY 240 GTCVSHVCAVFIYVFPFGISWVHRFSKRDSPLVILANTYLLVPPVNPVYGVYKKE 299
 DB 250 KICTSHLILVAMEVYPIIVSVTV-ALTTRIDNIRIINTALQTPIPMNPIIYLTKEE 308
 QY 300 IRORILRF-HV 310
 DB 309 VMQATLGLYKHI 320

RESULT 14
 S29711
 olfactory factor OR37 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
 C:Accession: S29711
 R:Ramung, K.; Krieger, J.; Strotmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.; Breer
 Nature 361, 353-356, 1999

A>Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273; PMID:7678922
A:Accession: S29711
A:Molecule type: mRNA
A:Residues: 1-305 <RAM>
C:Superfamily: olfactory receptor OR14

Query Match 25.9%; Score 418.5; DB 2; Length 305;
Best Local Similarity 32.5%; Pred. No. 1.5e-29;
Matches 100; Conservative 63; Mismatches 115; Indels 31; Gaps 5;

QY 15 ILILGLPELEAQLAPLPSLYIAVLGNLTIIVYRTHSHHEPMYIFLCMLSGIDIL 74
DB 1 LILGLSGPYKTEILYFIVLVMYLVHTGNGVLIISIFDSHLHTEMFELGLSLFDIC 60
QY 75 ISTSMPEMLAIFWFNSTTIOFDACLIQIFAIHSLGMESTVLLAAPRYVAICPHLH 134
DB 61 YTTSSVSTLVSLSKRNTSFGCTVOMFVGFAMSTBELGMAFDRVAICNPLRY 120
QY 135 ATVILTPVTKI-----GVAAYVRGAALMAPLPVFIKQLPFCRSNITLSHYCLADY 186
DB 121 SVMSKEVYVSMASWFSGINSVQTSIAM-----RLPFCGNVYNHPTCEVLAV 172
QY 187 MKLACDDIRVNVVYGLIIVISAIGLSLSPSYLLIKTVLGL-TREAQAKAFGCVSH 245
DB 173 LKLAGADISLNTVMTVSNAPFLVPLLFISYVILTYILKMSAGRRKAFSTCSAH 232
QY 246 VCAVFIYVPEIGLSMVRFSKRRDSP-----PVLANIYLLVPPVLPVPIYGVK 296
DB 233 LTVVVFYGTFSM-----YAKPKSODLTGKDKFGTSDKISLFYGVVTPMLNPIIYSR 287
QY 297 TKEIRORI 304
DB 288 NKDVKAAY 295

RESULT 15

S51356
A:Title: olfactory receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: S51356; S47014
R/Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
Eur. J. Biochem. 225, 1157-1168, 1994
A:Title: Olfactory receptor proteins. Expression, characterization and partial purification
A:Reference number: S51356; MUID:9504546; PMID:7957207
A:Accession: S51356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-309 <GAT>
A:Cross-references: EMBL:X80671; NID:9517365; PDB:CAAS6697.1; PID:9517366
R/Gat, U.; Nekrasova, E.; Lancet, D.; Natochin, M.
submitted to the EMBL Data Library, July 1994
A:Description: Olfactory receptor proteins: expression, characterization and partial purification
A:Reference number: S47014
A:Accession: S47014
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-309 <GAT>
A:Cross-references: EMBL:X80671; NID:9517365; PDB:CAAS6697.1; PID:9517366
C:Superfamily: olfactory receptor OR14

Query Match 25.9%; Score 418.5; DB 1; Length 309;
Best Local Similarity 33.0%; Pred. No. 1.6e-29;
Matches 104; Conservative 63; Mismatches 119; Indels 29; Gaps 8;

QY 6 GNSSATYFLLIGLPELEAQLAPLPSLYIAVLGNLTIIVYRTHSHHEPMYIFL 65
DB 5 GNSAVVVFVPLVGLTKQPELLPLFFLVLYLVTVGNGMLLIIVSPILHTEMYIFL 64
QY 66 CMLSGIDILISTSMPEMLAIFWFNSTTIOFDACLIQIFAIHSLGMESTVLLAAPRY 125
DB 65 SSLSFVDLCYSTVITRKMLVNFGLGRKRFITYSECMAQFFFPALFVTEGYLLTVMAVDYR 124

QY 126 VAICHPLEHATVLTLPVTYKIV-----AAVVRGAALMAPLPVFIKQLPFCRSNIT 176
DB 125 VAICRPLLYNVIMG-SRISCLVLVAFSLGLFSYVHTSAMM-----NLSFCKSYII 175
QY 177 SHSYCLHODVMKACDDIRVNVVYGLIIVISAIG--LDSILSPSYLLIKTVLGL-TRE 233
DB 176 SHYFDDALPLKLKACNTHNEL--LFIIGLNTLVPTLAVAISYVFIKSIIRISSE 233
QY 234 AQAKAFGTCVSHCAVFIY--VPIGLSMVRFSKRRDSPLPVLANIYLLVPPVLPV 291
DB 234 GRSYAFGTCSSHLMVAVGIFFGSITFMYLKSSNSLQEK-----VSSVFYTTVTPMLNPL 289
QY 292 VYGVTKETIRORILR 306
DB 290 IYSLRNDYKALGR 304

Search completed: February 9, 2004, 16:25:43
Job time : 21 secs

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: February 9, 2004, 16:05:17 ; Search time 163 Seconds
(without alignments)
8491.887 Million cell updates/sec

Title: US-10-017-066A-1

Perfect score: 3136
Sequence: 1 cagagagcgtatcttcagt.....aaaaaaaaaaaaaaaa 3136

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	377.4	12.0	963	4	US-09-439-313-526	Sequence 526, App
2	372.6	11.9	1474	1	US-08-465-980-1	Sequence 1, Appl1
3	372.6	11.9	1474	2	US-09-053-303-1	Sequence 1, Appl1
4	372.6	11.9	1474	4	US-09-339-115-1	Sequence 1, Appl1
5	372.6	11.9	1474	5	PCT-US95-07093-1	Sequence 1, Appl1
6	263	8.4	1539	4	US-09-668-680-13	Sequence 13, Appl1
7	215.4	6.9	231	4	US-09-439-313-462	Sequence 462, App
8	215.4	6.9	231	4	US-09-352-616A-462	Sequence 462, App
9	213.4	6.8	234	4	US-09-016-434-1047	Sequence 1047, App
10	134	4.3	1854	4	US-09-016-434-1312	Sequence 1312, App
11	125	4.0	1990	4	US-09-016-434-1056	Sequence 1056, App
12	121.4	3.9	1713	2	US-08-467-947A-1	Sequence 1, Appl1
13	121.4	3.9	1713	3	US-08-467-947A-1	Sequence 1, Appl1
14	120.2	3.8	3459	4	US-09-016-434-1363	Sequence 1363, App
15	112.6	3.6	251	4	US-09-439-313-352	Sequence 352, App
16	112.6	3.6	251	4	US-09-353-616A-352	Sequence 352, App
17	108.2	3.5	1060	4	US-09-668-680-10	Sequence 10, Appl1
18	104.4	3.3	1080	4	US-09-668-680-9	Sequence 9, Appl1
19	104	3.3	675	4	US-09-465-901-17	Sequence 17, Appl1
20	101.2	3.2	951	4	US-09-465-901-47	Sequence 47, Appl1
21	100.6	3.2	1297	4	US-09-668-680-11	Sequence 11, Appl1
22	96	3.1	945	4	US-09-016-434-1114	Sequence 1114, App
23	93.2	3.0	1282	4	US-09-016-434-1413	Sequence 1413, App
24	91.6	2.9	542	4	US-09-016-434-627	Sequence 627, App
25	86.6	2.8	666	3	US-08-748-506-8	Sequence 8, Appl1
26	86.4	2.8	669	4	US-09-465-901-25	Sequence 25, Appl1
27	83.2	2.7	1828	3	US-08-988-876-2	Sequence 2, Appl1

28	82.8	2.6	1438	4	US-09-016-434-1313	Sequence 1313, App
29	82	2.6	966	4	US-09-016-434-1372	Sequence 1372, App
30	81.8	2.6	945	3	US-08-748-506-7	Sequence 7, Appl1
31	81.6	2.6	952	4	US-09-016-434-1115	Sequence 1115, App
32	79.8	2.5	966	3	US-08-748-506-5	Sequence 5, Appl1
33	75	2.4	669	3	US-09-465-901-11	Sequence 11, Appl1
34	73.4	2.3	669	4	US-08-748-506-6	Sequence 6, Appl1
35	73	2.3	669	3	US-09-465-901-13	Sequence 13, Appl1
36	72.4	2.3	270	4	US-09-016-434-150	Sequence 150, App
37	71.2	2.3	666	4	US-09-465-901-13	Sequence 13, Appl1
38	70	2.2	648	4	US-09-016-434-1375	Sequence 1375, App
39	69.8	2.2	669	4	US-09-465-901-41	Sequence 41, Appl1
40	69	2.2	681	4	US-09-465-901-29	Sequence 29, Appl1
41	67.8	2.2	1525	3	US-09-157-603-4	Sequence 4, Appl1
42	67.8	2.2	1525	3	US-09-157-603-4	Sequence 4, Appl1
43	67.8	2.2	1525	4	US-09-587-436-4	Sequence 4, Appl1
44	67.4	2.1	1325	4	US-08-927-165A-4	Sequence 4, Appl1
45	67.4	2.1	3238	3	US-08-123-934A-5	Sequence 5, Appl1
				5	PCT-US94-10080-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-09-439-313-526
Sequence 526, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Milton, David C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Ranger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-526

Query Match 12.0%; Score 377.4; DB 4; Length 963;
Best Local Similarity 64.8%; Pred. No. 4,3e-82;
Matches 577; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY	171	CTTCATCTCAATAGAGCCCTGCTTGAAGAGGCTAGTTCTGAGCCCTCCATT	230
DB	30	CTTTGGCTTATGGATATCCAGATTAGAAGAACCATTTTCGGTGGCTTCCCT	89
QY	231	GTGCTCCCTTACCTTATTTGCTGCTAGAGTCAATCAATCAATTCATTTGCGGAC	290
DB	90	CTTTTCAGTATGATGAGTGGCAATTTTGAAGATCGATCGTCTTCATCGTAGAGC	149
QY	291	TGAGCAGACCTGCATGAGCCCATGATATATATTTCTTGACATGCTTGCAGCATGACAT	350
DB	150	GGAAGCAGCCCTGCAGCCCTCGATTTACTCTTCTCGACATGCTTGACCATGACCT	209
QY	351	CCTCATCTTCATCTTATTCATGATCCCAATATGCTGCGCATCTTCTGCTCAATTCACATAC	410
DB	210	GGCCTTATCCATCCATCCATGATCCCTTATCCCTTTCTGCTTGAATTTCCCGAGA	269
QY	411	CATCAGTTTATGCTTGTCTGCTACAGATTTTTCATCATTCTTATCTGACATGA	470

Db 270 GATTAGCTTTGAGGCGCTGTCTTACCAGATGTTCTTTATTCATGCGCCCTTCACGCAATTGA 329
 QY 471 ATCCACAGAGTGCCTGCTGGCCATGAGCTTTTGAACGGCATGTGGCCATCTGTACCCACATGGG 530
 Db 330 ATCCACGATCTGTCTGGCCATGAGCTTTTGAACGGCATGTGTATGTGGCCATCTGTACCCACATGGG 389
 QY 531 CCATGCCACAGTACTTACGTTGCTGTGTACCCAAATTGGTGTGCTGTGTGTGCG 590
 Db 390 CCATGTGCAAGTGTCTCAACAATACAGTAACAAGCCAGATTGGATCTGTGTGTGCG 449
 QY 591 GGGGGGTGCACTGATGGACACCCCTCTGCTCTTCAATCAAGAGAGTGGCCCTTGGCGGCTC 650
 Db 450 CGGATCCCTCTTTTTTTTCCCACTGCTCTGTGTATCAAGGGGTGGGCTTCTGTCCACTC 509
 QY 651 CAATATCTTTTCCCATCTCTACTGCTCAACCAAGATGTCAATGAAGTGGCTGTATGA 710
 Db 510 CAATATCTCTTGGCACTCTCTATTTGTATCCACAGAGTGTATGAAGTGGCTATGACAG 569
 QY 711 TATCCGGGTCAATGTGTGTATGTGGCTTATGTATCATCTCCGCAATGTGGCTGTACACTC 770
 Db 570 CACTTTGCCCAATGTGTATGTGTCTTACTGTCACTTGTGTGTATGTGGCTGTACACTC 629
 QY 771 ACTTCTCATCTCTCTCTCAATCTGTCTTATTTCTTAAACATGTGTGGGCTTGAACAGTGA 830
 Db 630 AATGTTCACTCTCTGTCTCTCTATTTCTATATACGAACGGTTCGTGCATCTGTCCAA 689
 QY 831 ---AGCCACAGGCGCAAGCAATTTGGGCACTTGGGCTCTCATGTGTGTGTGTCTTCAATT 887
 Db 690 GTACAGAGCGGCGCAAGGCTTTGGAACCTGTGTCAACATGTGTGTATCTGCGCTT 749
 QY 888 CTATGTACTTTCAATTGTGATGTGTCCATGTGTGATCTGCTTTAGCAAGCGGCGTACTCTCC 947
 Db 750 CTATGTGCCACATTAATGGGCTCTCTCAATGTGTACACCGCTTGGAAACAGCCTTATCCCAT 809
 QY 948 GCTGCCCGTCACTTTGGCCCAATATCTATCTGTGTGTCTCTGTGTGTCAACCCATTTGT 1007
 Db 810 TGTGCTGT 869
 QY 1008 CTATGAGTGAAGACCAAGAGATTGACAGCGGATCTTGCATTTTCCA 1058
 Db 870 CTATGTGTGCCAAACCAACCAAGATCAGAACACGGGTCTGGCTATGTGTCA 920

RESULT 2
 US-08-465-980-1
 Sequence 1, Application US/08465980
 Patent No. 5756309
 GENERAL INFORMATION:
 APPLICANT: Soppet, Daniel R.
 APPLICANT: Li, Yi
 APPLICANT: Rosen, Craig A.
 APPLICANT: Ruben, Steven M.
 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 City: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465,980
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:

	NAME:	Ferraro, Gregory D.
	REGISTRATION NUMBER: <td>36,134</td>	36,134
	REFERENCE/DOCKET NUMBER: <td>325800-446</td>	325800-446
	TELECOMMUNICATION INFORMATION: <td></td>	
	TELEPHONE: <td>201-994-1700</td>	201-994-1700
	TELEFAX: <td>201-994-1744</td>	201-994-1744
	INFORMATION FOR SEQ ID NO: <td>1:</td>	1:
	SEQUENCE CHARACTERISTICS: <td></td>	
	LENGTH: <td>1474 base pairs</td>	1474 base pairs
	TYPE: <td>nucleic acid</td>	nucleic acid
	STRANDEDNESS: <td>single</td>	single
	TOPOLOGY: <td>linear</td>	linear
	MOLECULE TYPE: <td>CDNA</td>	CDNA
	FEATURES: <td></td>	
	NAME/KEY: <td>CDS</td>	CDS
	LOCATION: <td>274..1233</td>	274..1233
	US-08-465-980-1	
	Query Match	11.9% Score 372.6; DB 1; Length 1474;
	Best Local Similarity	64.4% Pred. No. 7.7e-81;
	Matches	574; Conservative 0; Mismatches 314; Indels 3; Gaps 1
Qy	171	CTTCATCTTAATAGACCTCCCTGGTTTAAAGAGAGCTCAGTTCTGGTGGCCCTTCCATT
Db	303	CTGTGTGCTATTGTATGCCAGGATTAGAAAGCCATTCTGGTGGCTTCCCT
Qy	231	GTGTCCTCTTACTTATTTGTGTGCTAGGTAACTTGACATTCATCTCATTTGTGGGAC
Db	363	CTTTCCATGTATGTAGTGGCAATGTGTGAACTGCATCGTGGCTTTCATGTAAAGAC
Qy	291	TGAGCAGAGCCTGCATGAGCCCATGTATATATTTCTTTCATGCTTTCAGGATTGACAT
Db	423	GGAAGCAGCCTGCATGAGCTCCGATGTACTCTTTCTGTGATGCTTGACGACATTGACCT
Qy	351	CCTATCTCCACCTTCATCCATGAGCCCAAAATGTGGCCATCTTCTGTGTTCAATCCACTAC
Db	483	GGCCTTATCCACATCCACCATGCTTAAGATCTTGCCCTTTCGTGTGTTGATCCCGAGA
Qy	411	CATCCAGTTGATCTGTCTGTGCTACAGATTTTTCGATCCATCCATCTTATCTGAGATGA
Db	543	GATTAGCATTTAGGCTGTCTTTTACCCAGATGTTCTTATTCATGACCCCTCAGCATTGA
Qy	471	ATCCAGAGTGTGTGTGGCAATGCTTTTGAACCGCTATGTGGCCATCTGTCAACCATGGG
Db	603	ATCCACATCTGTGTGGCAATGCTTTTGAACCGCTATGTGGCCATCTGTCAACCATGGG
Qy	531	CCATGCCACAGTACTTACGTTGACCTGTGTCACCAAAATGGATGGCTGTGCTGTGGTCG
Db	663	CCATGTGTCAGTGTCTCAACAAATACATGACAGCCCAATGGATGGATCGTGTGTGTCG
Qy	591	GGGGGCTGCATGTATGGACACCCCTTCCCTGTCTTATCAAGAGAGTGGCCCTTCCGGCTC
Db	723	CGGATCCCTCTTTTTCCTCCATGCTCTGTCTATCAAGGGGCTTGGCTTGTGCATCTC
Qy	651	CAATATCTCTTCCATTCTTACTGCTTATCTTAAAGACTGTGTGGCTTGAACGTGA
Db	783	CAATGTCTCTGCGACCTTATGTGTCCACCAAGATGATGAAGTTGAGCTTATGACGA
Qy	711	TATCCGGGTCAATGTGTGCTATGAGCCCTTATCTGTATCATCTCCGCCATTTGGCCCTGATC
Db	843	CATTTTGCCCAATGTGTGCTATGAGCCCTTATCTGTATCATCTCCGCCATTTGGCCCTGATC
Qy	771	ACTTCTCATCTCTCTTCATATCTGCTTATCTTAAAGACTGTGTGGCTTGAACGTGA
Db	903	AATGTTCATCTCTCTGCTTATCTTATCTTGAATATGCAAGCGTTCGTGCAACGTCTTCCAA
Qy	831	---AGCCAGAGCCAGGCAATTGGCACTTGGCTGTCTCATGTGTGCTGTGCTCATATT
Db	963	GTCAGAGCGGCGCCAGGCTTTTGAACCTGTGTGTCAACATTTGTGTGTGTGTGTGTGCTT
Qy	888	CTATGTACTTTTCATTTGATTTGTCATGATGTGCATGTGCTTTAGCAAGCGGCTGACTCTCC
Db	1023	CTATGTGCTCACTTATTTGCTCTGATTTGTAACACCGCTTTGAAACAGCCCTTATCCAT

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,115
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/053,303
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 274..1233
US-09-339-115-1

Query Match 11.9%; Score 372.6; DB 4; Length 1474;
Best Local Similarity 64.4%; Pred. No. 7.7e-81;
Matches 574; Conservative 0; Mismatches 314; Indels 3; Gaps 1;

QY 171 CTTCATCTCAATGAGGCTGCTTGAAGAGGCTGCTGCTTGGCTTCCCAT 230
DB 303 CTGTGCTTATGTATGCCAGATTAGAAAGCCATTCTGGGTTGCCCT 362
QY 231 GTGCTCCCTTACCTTATGCTGTAGTAACTTGAATCATCATCATGTCGGAG 290
DB 363 CTTTCCATGTATGTATGTCAGATGTGTGAATGCAACGATCTTCACTGAAGAC 422
QY 291 TGAGCAGAGCTTGCATGAGCCCATGTATATTTCTTGCATGCTTTCAGGATGACAT 350
DB 423 GGAACGAGAGCTTGCAGCTCCGATGTACCTCTTCTGCAATGCTTTCAGGATGACAT 482
QY 351 CCTCATCTCAGCTCATGCTTGCATGAGCAAAATGCTGAGCATCTTGTGATTCACATAC 410
DB 483 GAGCTTATCCATCCATCCATGCTTGAATCCTTGTGCTTCTGCTTGTGATTCGAGAG 542
QY 411 CATTCAGTTGATGCTTGTCTGTCTACAGATTTTGGCATCACTCTTATCTGGAGTGA 470
DB 543 GATTAGCATTTGAGGCTGTCTTACCCAGATGTTCTTATTCATGCCCTTCAGCATTTGA 602
QY 471 ATCCAGAGTCTGCTGGCCATGCTTTTGAAGGCTATGTGGCATCTGTCACCACTGGG 530
DB 603 ATCCAGATCTTCTGCTGCAATGAGCTTTTGAAGGCTATGTGGCATCTGTCACCACTGGG 662
QY 531 CATTCAGAGTATGCTTGTCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
DB 663 CCATGCTGAGTGTCTCAAAATACAGTAAACAGCCAGATGTCATGCTGCTGCTGCTGCTG 722
QY 591 GGGGGGCTGCTGATGAGCAAGCCCTTGTCTGCTTCAATGAGCAAGCTGCTTGTGCGCTG 650
DB 723 CGGATCTCTTTTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
QY 651 CAATATCTTCTTCCATCTCTATGCTTCAACCAAGATGCTGATGAGCTGCTGCTGATGA 710
DB 783 CAATATCTTCTTCCATCTCTATGCTTCAACCAAGATGCTGATGAGCTGCTGCTGATGA 842
QY 711 TATCCGGGTAAATGTGTCTATGCTTATGCTGATCATCTCCGATGCTGCTGCTGCTGCTG 770
DB 843 CACTTGTCCCAATGTGTATGTGTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902

QY 771 ACTTCTATCTCTCTCTCATATCTGCTTATCTTAAAGCTGTGTGGCTTGAACAGTGA 830
DB 903 AATGTATCTCTCTCTCTCTATTTCTGATTAATACAGAGGTTCTGCACTGCTTCCAA 962
QY 831 ---AGCCAGAGCCCAAGGATTTGGCACTTGGCTCTCTCATGTGTGTCTGTCTCATATT 887
DB 963 GTGAGAGCGGCGCAAGGCTTTGAACTGTGTGTACACATTTGTGTGTGTGTGTGTGTGT 1022
QY 888 CTATGATCTTTCATTTGATGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 947
DB 1023 CTATGTCGATTTATGAGCTCTCAGTTGTATACCGCTTTGAAAACAGCCTTATCCAT 1082
QY 948 GCTGCCGCTATCTTGGCCATATCTATCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1007
DB 1083 TGTGCGGTGTGTATGATGTCATCTTACCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1142
QY 1008 CTATGAGTGAAGACAAGAGATTTGACAGCGCATCTTGCATTTTCCA 1058
DB 1143 CTATGTCGCAAAACCAAGATGACAGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1193

RESULT 5

PCT-US95-07093-1
Sequence 1, Application PC/TUS9507093
GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.
APPLICANT: Li, Yi
APPLICANT: Rosen, Craig A.

APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSER: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07093
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 274..1233
PCT-US95-07093-1

Query Match 11.9%; Score 372.6; DB 5; Length 1474;
Best Local Similarity 64.4%; Pred. No. 7.7e-81;
Matches 574; Conservative 0; Mismatches 314; Indels 3; Gaps 1;


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QY 171 CTTCATCCCTAATAGGCTCCCTGGTTTGAAGAGGCTCAGTTCGTGGCCCTCCAT 230
Db 303 CTGTGTGCTTATGATGATCCAGATTTAGAGAAAGCCATTTCTGGGTGGCTCCCT 362
QY 221 GTGCTCCCTTACCTTATTTGCTGTGCTAGTAAGTACATCATCTACATTTGGCGAC 290
Db 363 CTTTCCATGATGATGAGGGAATGTGGAAGATGATGCTGTGCTTCACTGTAAGAGAC 422
QY 291 TGAGCAGAGCCCTGATGAGCCCATGTATATTTCTTTCAGTTCAGGATTCAGAT 350
Db 423 GGAAGAGAGCCCTGACGCTCCGATTAACCTCTTCTGCAATGCTGAGGATTAACCT 482
QY 351 CCTCATCTCCACCTTCATCATGAGCAAAATGCTGCCATCTTCTGTTCATTCCTAC 410
Db 483 GGCCTTATCCACATCCACCATGCTTACATCTTCCCTTCTGCTTGAATCCCGAGA 542
QY 411 CATCCAGTTTATGCTGTGCTGCTAAGATTTTGGCCATCCATCTTATCTGGCATGA 470
Db 543 GATTAGCATTTAGGCTGCTTCTTACCAAGATTTCTTATATGCTCCCTCTGAGCATTTGA 602
QY 471 ATCCACAGTCTGTGCTGCTGCTTTCAGCCGATGCTGCTGCTGCTGCTGCTGCTGCT 530
Db 603 ATCCACATCCCTGCTGCTGCTGCTGCTTTCAGCTTATGCTGCTGCTGCTGCTGCTGCT 662
QY 531 CCATGCCACAGTACTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
Db 663 CCATGCTGAGTGTCAACATTAACATTAACATTAACATTAACATTAACATTAACATTAAC 722
QY 591 GGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
Db 723 CGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
QY 651 CAATATCTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 710
Db 783 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 842
QY 711 TATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
Db 843 CACTTGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902
QY 771 ACTTGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830
Db 903 AATGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 962
QY 831 ---AGCCAGGCAAGGCAATTTGGCACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
Db 963 GTCAAGAGGCGGCAAGGCTTTCGAACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1022
QY 888 CTATGTACCTTTCATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 947
Db 1023 CTATGTGCACTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
QY 948 GCTGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
Db 1083 TGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1142
QY 1008 CTATGAGTGAAGACAAAGAGATTCAGACGAGCATTCCTTGACCTTTTCCA 1058
Db 1143 CTATGCTGCAAAACCAACAGATCAGAACACGGGTGCTGCTGCTGCTGCTGCTGCTGCT 1193

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RESULT 6
US-09-668-680-13
Sequence 13, Application US/09668680

Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui

```

APPLICANT: Xue, Aidong J.  
APPLICANT: Xu, Chongjun  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6436703el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 790CIP2A  
CURRENT APPLICATION NUMBER: US/09/668,680  
CURRENT FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: pl_genes Version 2.0  
SEQ ID NO: 13  
LENGTH: 1539  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (130)..(1539)  
US-09-668-680-13

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Query Match 8.4%; Score 263; DB 4; Length 1539;
Best Local Similarity 57.6%; Pred. No. 38-54;
Matches 511; Conservative 0; Mismatches 370; Indels 6; Gaps 2;

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QY 183 AGGCTCCCTGCTTGAAGAGGCTCAGTTCGTGGCTTCCATTTGCTCCCTCTTA 242
Db 636 AGGATCCCAAGAGGCTGAGGCTCCCTCCTTCTGATTCGATCCCTTCTGTCATGTA 695
QY 243 CCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 696 TCTTTGAGCACTGTGGAATGCTGCTCCTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 755
QY 303 GATGAGCCCATGTATATTTCTTTCAGTTCAGGATTCATTCCTGCTGCTGCTGCTGCT 362
Db 756 TATGACCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
QY 363 CTCATCCATGCCCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 816 TACATGCTGCCCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
QY 423 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
Db 876 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
QY 483 GCTGCGCATGCTTTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db 936 ACTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 995
QY 543 ACTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
Db 996 TCTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
QY 603 GATGAGACCCCTTCTGCTTCAATCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
Db 1056 TGTCTCCCTTCACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1115
QY 663 CCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
Db 1116 ACACATATCTGAGCAATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1175
QY 723 TGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
Db 1176 TATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1235
QY 783 CTTCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
Db 1236 CATTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1295
QY 840 CAGGCAATTTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899

```


INFORMATION FOR SEQ ID NO: 1047:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNUT01
CLONE: 998550
US-09-016-434-1047

Query Match 6.8%; Score 213.4; DB 4; Length 234;
Best Local Similarity 96.4%; Pred. No. 1.3e-42;
Matches 214; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 334 CTTTCAGGATGACATCTCTATCTCCACCTCATCATGAGCCAAATGCTGGCATCTC 393
DB 1 CTTTCAGGATGACATCTCTATCTCCACCTCATCATGAGCCAAATGCTGGCATCTC 60
QY 394 TGGTTCATTCCTACCTACCTGATTTGATGCTTCTCTGCTACAGATTTTGGCATCCAC 453
DB 61 TGGTTCATTCCTACCTACCTGATTTGATGCTTCTCTGCTACAGATTTTGGCATCCAC 120
QY 454 TCCCTATCTGAGTGAATCCACAGTCTGCTGGCATGCTTTGACCGCTATGTGACC 513
DB 121 TCCCTATCTGAGTGAATCCACAGTCTGCTGGCATGCTTTGACCGCTATGTGACC 180
QY 514 ATCTGTACCCACCTGCGCCATGCGACAGTACTTACCTGCT 555
DB 181 ATCTGTACCCACCTGCGCCATGCGACAGTACTTACCTGCT 222

RESULT 10

US-09-016-434-1312
Sequence 1312, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1312:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 932085
US-09-016-434-1312

Query Match 4.3%; Score 134; DB 4; Length 1854;
Best Local Similarity 48.6%; Pred. No. 6.3e-23;
Matches 430; Conservative 0; Mismatches 445; Indels 9; Gaps 2;

QY 151 AATGATCCAGTGTACATCTTCAATCCATAAGGCTCCCTGGTTAGAAAGGTGAC 210
DB 332 AATCAACACAGATCTCAACATCTCCCTGCGGCTGGCCATCCACACAGAGACA 391
QY 211 TTCTGTGGCTTCCCATGCTGCTCCCTCACTTATGCTGTGAGTAACTTGACA 270
DB 392 AACCTGTGATGAGCCCTGTCTTGGCATGATCTTACACACCTCCTGAGGAACTCCTC 451
QY 271 ATCATCTACATTTGGGAGCTAGACACAGCTGTGATGAGCCCATGTATATTTCTTGC 330
DB 452 ATCATGTCTCTATGACGTGACATCCCATCCACACAGCTATGATATTTCTTCACG 511
QY 331 ATGCTTTCAGGATGACATCTTCAATCTCCACTCATTCATGAGCCAAATGCTGGCATC 390
DB 512 AACTTGTCTCTCTGACCTTCTGCTTCTTCTGAGACCTATCCAGTTGTACAGAAC 571
QY 391 TTCTGTCAATTCACATCCATCCAGTGTGATGCTGTGCTGCTACAGATTTTGGCATC 450
DB 572 ATGCAACACAGAGACCATCCATCCCTATGCGGACTGCTGACCAATGACTTCTTC 631
QY 451 CACTCCTTATCTGAGATGATCCACAGTGTGCTGGCCATGCTTGAACGGTATGTC 510
DB 632 CTGTATTTGAGAACCTGAGAGCTTCTCTTGTGGCCATGAGCTATGACCGTATGTC 691
QY 511 GCCATCTACACCACTGCGCCATGCGACAGTACTTACCTGCTGTGTGTCACCAAAAT 570
DB 692 GCCATCTGCTCCCTGACATACACCGCATCATGAGCCCATGCTGTGTGCTGCGCC 751
QY 571 GGTGTGCTGTGTGTGTGGGGGGGTGTGATGTAGAGCAACCCCTTCCTTCAACAG 630
DB 752 GTGGCGCTGTCTGGGTGTGACACCTTCCATGCCATTTACACTTACTCAAGGCC 811
QY 631 CAGTCCCTTCTGCGGCTCCAAATCTTCCATTTCTTACTGCTACCAACAATGTC 690
DB 812 AGGTGTGTTTGTGACAGACATGATGCCCATTTTCTGTGATATGTGCTGTG 871
QY 691 ATGAAGCTGCTGTGATGATATCCGGGTCAATGTGCTATGAGCTTATGCTCATATC 750
DB 872 CTGAAGCTGCGCTTCTGTGACACTGAGTATGATGAGGTATATTTATCATGAGAGG 931
QY 751 TCGGCATTTGGCGTGTGACTCATCTCTCTCATCTGCTTATCTTAAAGT 810
DB 932 CTCTATCTGTGATCCCATCTTACTCATCTTGGGTCTATGCAAGATTTCTCTC 991
QY 811 GTGTT--GGGCTTGAACAGTAAAGCCAGGCAAGGCTTGGCATTTGGCATTTGCTGTCTAT 867
DB 992 ATCTCTAAGAGTCCCTTCTCTTAAGGTATCTGCAAGGCTTCTCTAATTTGTGCTCCAC 1051
QY 868 GTGTGTGCTGTGATATTTATGATGATCTTCAATGATGATGATGATGATGATGATGAT 927
DB 1052 CTGTCTGTGTGATCTGCTCTATGATGATGATGATGATGATGATGATGATGATGAT 1105
QY 928 AGCAAGGCGGTGATCTGCGCTGCGCTGATCTTGGCCATATCTATCTGTGCTTCT 987
DB 1106 TCACTAATAGTTTCACTTAAGAGACTGTGATGATGATGATGATGATGATGATGAT 1165
QY 988 CCTGTGCTCAACCAATGTCTATGAGTGAAGAGACAAAGAGAT 1031
DB 1166 CCAATGCTAACCCTTATCTTACAGCTGAGGAACAGAGAT 1209

RESULT 11

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STERNE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1713 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 116..1003
 US-08-467-947A-1

Query Match 3.9%; Score 121.4; DB 2; Length 1713;
 Best Local Similarity 48.0%; Pred. No. 6.9e-20;
 Matches 378; Conservative 0; Mismatches 406; Indels 3; Gaps 1;

151 ATGAATCCAGTGTACATCTTCAATGAGCTCCCTGTTGAAAGAGGCTCAG 210
 137 AATCAGACAAATGGTACAGAGTCTCTACATGAGATTTCGCGCCCAAGATTCAG 196
 211 TTCTGGTGGCTTCCCATGTCGCTCCCTACCTATTCGTCGTCAGTACATGACA 270
 197 ATGCTCTCTTTGGGCTCTTCTCCCTGTTCTATGCTTCACCTGCTGGGAAGGAGCC 256
 271 ATCATCTACATTTGGGAGTACAGACAGCCCTGATGAGCCATGATATATTTCTTGC 330
 257 ATCTGGGGCTCATCTCATGTGACATCCAGATCCACACCCCATGATCTTCTCTGCA 316
 331 ATGCTTTCAGCATGATCTCTCATCTCCACTCATCCAGTCCCAAAATCTGGCCATC 390
 317 CACCTGGCGGTGTAACATGCTGATGCTGCAACACAGTCCCAATCTGATGAC 376
 391 TTCTGTTCAATTCACATCAACATCCAGTTTGAATGCTGTCGTCACAGATTTTGGCATC 450
 377 CTCCTGACATCCAGCCAGCCATCTCTTGTGTCGTCATGACATCTTCTCTT 436
 451 CACTCTTATTTGGGATGGAATCCACAGTCTGCTGGCCATGAGCTTTGACCCATATG 510
 437 TTGAGTTTGGACATGTAATGCTCTCTGTTGTCGTCATGATCTTACATCGGATG 496
 511 GGCATCTGTCACCACTGCGCCATGACACAGTACTAGTTCCTCGTGCATCCAAAT 570
 497 GGCATCTGTCACCTCTCGATATTTTCAATCAAGACTGGAAGTCTGATCACTGTG 556
 571 GGTGTGCTGCTGTGTCGCGGCTGTCATGATGCAACCCCTTCTGCTTCAAG 630
 557 GGCATCACTCTGTCATGATGTCCTCCCTGCTGCTGATGTCATGATGATCTCTCA 616
 631 CAGCTGCTCTGCGCGCTCCAAATACCTTCCCATCTTCTGCTTACACCAAGATG 690
 617 AGACTGCTCTTTTGGGCTCTGTAATCAACCACTTCTTGTGAAATCTGCTGTC 676
 691 ATGAAGTGGCTGTGATGATATCCGGATCAATGTCGTATAGGCTTATGCTATC 750
 677 CTCAGGCTGGCTGTGATGATGCTGCTCAACAGTGTGATCTTGAAGCTGCTATG 736
 751 TCCGCAAT---GGCTGATCTCATCTCTCTCTCAATCTGATCTTATTTTAA 807
 737 TTATCTGATGAGCACTGCTGCTGCTGCTGCTCTCTCTCTCAACATCTTGGGAG 796
 808 ACTGTGTGGCTTGAACATGTAAGCCCAAGGCAAGGCAATTTGGCACTTGGCTCTCAT 867

DB 797 ATCTGAGATCCAGTCTGGGAGGCGCCAGAAAAGCCCTTCTCCACTCTCTCCAC 856
 QY 868 GTGTGCTGTGTGATATTTATGATGATCTTCAATGATGTCATGTCATGCTTT 927
 DB 857 CTCGTGCTATGGAGACTCTTCTTGGAGCGCCATGCTATGATGAGCCCTTAAGTCC 916
 QY 928 AGCAAGC 934
 DB 917 CGCCATC 923

RESULT 13

US-08-467-947A-1
 ; Sequence 1, Application US/08467947A
 ; Patent No. 6090575
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; APPLICANT: CAO, LIANG
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER
 ; APPLICANT: BULT, CAROL J.
 ; APPLICANT: SUTTON III, GRANGER G.
 ; APPLICANT: ROSEN, CRAIG A.
 ; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 ; TITLE OF INVENTION: Coupled Receptor GPR1
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVE., NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,947A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/04079
 ; FILING DATE: 30-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STERNE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 1:
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 ; STRANDEDNESS: both
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 ; US-08-467-947A-1

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 211 TTCTGGTGGCTTCCCATGTCGCTCCCTACCTATTCGTCGTCAGTACATGACA 270